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OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ω.	P02730 homo sapien	2 rattu		P15575 gallus gall				P48746 oryctolagus		P16283 mus musculu	P23348 rattus norv		018917 oryctolagus		Q9gkyl oryctolagus			Q96q91 homo sapien		P51556 rattus norv		_			mycok		4 schiz		P14176 escherichia	P23134 rhodospiril	03603	N	PO4185 sus scrofa
	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3AT_ONCMY	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	B3A2_CAVPO	B3A4_RABIT	LIPA_MYCLE	B3A4_RAT	B3A4_HUMAN	COBK_METTH	KDGA_RAT	KDGA_MOUSE	C13A_MYCTU	SL11_HUMAN	NU3M_HYLLA	LIPA_MYCTU	UROK_HUMAN	YKT5_SCHPO	NRFE_ECOLI	PROW_ECOLI	CYB_RHORU	KDGL_CAEEL	HEM3_CAUCR	UROK_PIG
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VM2_REOVD	KDGA_PIG	LIFR_MOUSE	POLG_BOVEV	CLR3_MOUSE	CLR3_HUMAN	CLR3_RAT	SC31_RAT	YC56_PORPU	COXX_RHOSH	CBP1_HORVU	HLYB_SERMA	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID=10116;
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kudrycki K.E., Shull G.E.;
Kudrycki K.E., Shull G.E.;
"Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
                                                           ö
     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00219; ANION EXCRANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
  ; DB 1;
4.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                      927 AA.
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
100.0%; Score 104;
100.0%; Pred. No. 4
:1ve 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Erythrocyte;
IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
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EMBL; L02943; AAA40801.1; -.
PIR; A33810; A33810.
HSSP; P02730; LBTS.
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Kidney;
MEDLINE-89255254; PubMed-2722777;
                                                                                                                                       720 GMPWLSATTVRSVTHANALT 739
                                                                                                              1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                            20, Created)
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                                             Conservative
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                                                                                                                                                                                                                                                                                                      STANDARD;
                            Local Similarity
nes 20; Conser
                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel.
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  Query Match
                                 Best Loc
Matches
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SEQUENCE FROM N.A. MEDAMED 110791;
MEDILTE-6826011; PubMed-2410791;
Kopito R.R., Lodish H.F.;
"Primary structure and transmembrane orientation of the murine anion
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1). (AE 1)
                                                                                                                                                                                                   PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
/Frid-VSP_000455
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                                                                                                                                                                                                                                                                          Length 927;
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                                                                                         EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                                                                                                                     EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                681A228474E5E9DE CRC64;
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native splicing.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86634211; Pubwed-3840489;
ROPITO R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                        100.0%; Score 104; DB 1; 100.0%; Pred. No. 4.4e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                    929 AA.
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                                                         POTENTIAL. POTENTIAL.
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  Alternative
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MEDLINE-86274622; Pubmed-3015590;
                                                                                                                                                                                                                                                                                                                      1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                                                                                                                                   927 AA; 103172 MW;
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Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                 Conservative
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 Palmitate;
            420
927
441
473
496
527
528
585
604
619
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Best Local Similarity
Matches 20; Conserv
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 Lipoprotein;
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P04919;
                        DOMAIN
TRANSMEM
                                                                   TRANSMEM
                                                                                                    FRANSMEM
                                                                                                                           FRANSMEM
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            DOMAIN
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                                                                                                                                                                                                               HEMOGLOBIN.
SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                              ACROSS
                                                                                                                   "Major proteclytic fragments of the murine band 3 protein as obtained after in situ proteclysis."; Blochim. Biophys. Acta 980:291-298(1989).
                                                                                 MEDLINE-89229233; PubMed-2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
                                                                                                                                                   1- FONCTION: BADD 3 IS THE MAJOR INTEGRAL GIXCOPROTEIN OF THE ERYPHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1.1. EXCHANGE OF INDRGANIC ANIONS ACT THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
            Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P027314; A2314.

HSSP, P027314; A2314.

HSSP, P02730; 1BTS

MGD; MGI: 109393; SI-da1.

InterPro; IPR003020; HC03_cotranspt.

Ffam; PF00555; HC03_cotranspt.

FTGFRAMS; TGR00834; ac; 1.

R PROSITE; PS00219; ANION_EXCHANGER_1; 1.

R PROSITE; PS00220; ANION_EXCHANGER_2; 1.

R TGRAMS; TGR00830; ANION_EXCHANGER_2; 1.

R TGRAMS; TGR00830; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                    ISOId=P04919-2; Sequence-VSP_000454;
TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein; Palmitate; Alternative splicing.

DOMAIN 1 222 CYTOPLASMIC (POTENTIAL).

DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms-2;
                                                                     SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed=2713407;
                                                                                                                                                                                                                                                                                   Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
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EMBL; M29379; AAA37187.1; --
EMBL; J02756; AAA37278.1; --
EMBL; X03917; CAA27555.1; --
                                   band 3-<u>like protein.";</u>
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4443
475
475
529
560
606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SÜBÜNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- TISSÜE SPECIFICITY: BRYTHROCYTE.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-89039870; PubMed-3185555;

Kim H.R.C., Yew N.S., Ansorge W., Schwager C.,

Kim H.R.C., Yew N.S., Ansorge W.D.;

Wennstroem B., Zenke M., Engel J.D.;

"Two different mRNAs are transcribed from a single genomic locus encoding the chicken erythrocyte anion transport proteins (band 3).";

Mol. Cell. Biol. 8:4416-4424(1988).

I-FUNCTION: BAND 31S THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS INTES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Band 3 anion transport protein.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                             ;
0
                                                                                                                                                       Length 929;
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PROSTITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
Transmembrane; Glycoprotein; CTTOPLASMIC (POTENTIAL).
CTTOPLASMIC (POTENTIAL).
                           Missing (in isoform Kidney).
/FIId-VSD-000454.
G -> S (IN REF 5).
V; 5C0R281C394FB614 CRC64;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE (ANION EXCHANGE).
     PALMITATE (BY SIMILARITY).
                                                                                                                                                       100.0%; Score 104; DB 1; 100.0%; Pred. No. 4.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 922 AA.
                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. POTENTIAL.
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                            GMPWLSATTVRSVTHANALT 757
                                                                                                                                                                                                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                         103135 MW;
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                                                                                                                                                          Query Match 100.0
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
861
79
                                                                                 467
                                                                              467 4
929 AA;
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  861
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P15575;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
B3AT_CHICK
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WEDLINE-9234456; PubMed-1637296;
WEDLINE-923456; PubMed-1637296;
WEDLINE-923456;
WEDLINE-92345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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OMAIN 393 918 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (PROBABLE).
; FF4ECAD6D60CF0CF CRC64;
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                     Score 100; DB 1; Length 922;
Pred. No. 2e-08;
                                                                                            EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                        0; Indels
  EXOPLASMIC LOOP (POTENTIAL)
                                              CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 AA.
                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                             POTENTIAL.
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HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
TotorPro; IPR003020; HC03_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                               1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
                                                                                                                                                                                                                                                           102223 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Band 3 anion exchange protein.
                                                                                                                                                                                                                                                                                                          96.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                      635
671
691
730
791
817
817
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                                                                                                                                                                                                                                                              922 AA;
                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                   TRANSMEM
DOMAIN
TRANSMEM
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CARBOHYD
SEQUENCE
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TRANSMEM
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Stomach;
MEDILINE-90094439; PubMed-2294114;
Rudryckí K.E., Newman P.R., Shull G.E.;
Rudryckí K.E., Newman G.E.;
Figh cloning and tissue distribution of mRRNAs for two proteins that are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1991 (Rel. 20, Last Sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
); 37E163141FBDC16A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90319095; PubMed-2371270;
Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                        Score 95; DB 1; Length 918; Pred. No. 1.3e-07;
                                                                      EXOPLASMIC LOOP (POTENTIAL)
                                                                                                               POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                   PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                  POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                   1; Mismatches
                              POTENTIAL
                                                         POTENTIAL
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                                           POTENTIAL
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                                                                                                                                                                                                                                                             101893 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                        Query Match 91.3%;
Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J05166; AAA40799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat)
                                                                                                                                                                                                                                              568
918 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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DOMAIN
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SEQUENCE
TRANSMEM
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Name=B1;
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CARBOHYD
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VARSPLIC
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EMBL;
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P13808; Q9ES09; Q9ES10; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLGAA OR AE2.
Buks musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A).

MEDLINE-88034212; PubMed-3182834;

Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;

"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";

"I shol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE-20462926, Pubmed-11006093. Lecanda J., Urtasun R., Medina J.F.; Medina J.F.; Medina J.F.; Mojecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 93; DB 1; Length 1234; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                  POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; · Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136635 MW; FAB4ED12BB916216 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALMITATE (BY SIMILARITY).
G -> A (IN REF. 2).
                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                      HIS-RICH.
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31ochem. Biophys. Res. Commun. 276:117-124(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                             TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                    POTENTIAL.
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                        HSSF, FULLY, LOSSEL PRODICATION OF CHANGE.
INTERPRO; IPRODICATION HCO3_cotranspt.
Pfam: PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 85.0
17; Conservative
PIR; A34911; A34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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CARBOHYD
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DOR NO DO
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                                                                                                                                                                                                                                                                                                                                                                                         Isoid-P13808-5; Sequence-VSP_000459, VSP_000461;
-! TISSUE SPECIFICITY: Isoform a 1s widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Glycoprofein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

DOMAIN 1 703 CYTOPLASMIC (POTENTIAL).

MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . . .) (POTENTIAL). . . .) (POTENTIAL). . . .) (POTENTIAL).
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EXOPLASMIC LOOP (POTENTIAL)
  Q.
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PALMITATE (BY SIMILARITY)
MSSAPRRPASGADSLHT -> MDF1
FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                  SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                Event-Alternative splicing; Named isoforms-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B2).
/FTId-VSP_000457
                                                                                                                                                                                                                                                                                     IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                                                                                          IsoId-P13808-4; Sequence-VSP_000460;
                                                                                                                                                                                                                          IsoId=P13808-2; Sequence=VSP_000458;
                                                                                                                                                                  IsoId-P13808-1; Sequence-Displayed;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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MGD, MGI:109351; S1c4a2.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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AP255774; AAG23155.1; -...
AP255774; AAG23156.1; -...
AP255774; AAG23158.1; -...
AP255774; AAG23157.1; -...
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EMBL; AF255774; AAG23158.1; -
PIR; A31789; A31789.
HSSP; P02730: 1 mm
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914
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 Total number of hits satisfying chosen parameters: 127863 seqs, 47026705 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ptio	P02730 homo sapien		mus mus			-		homo s	gallu		P16283 mus musculu	P23348 rattus norv	P48751 homo sapien		_	_	P14914 rickettsia	н	P19338 homo sapien				Q8uey3 agrobacter1	-	P33025 escherichia	_	Q10821 mycobacteri	_	_	P54189 plasmodium	_	18	969
SUMMARIES		ΩI	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3AT_CHICK	B3AT_ONCMY	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	Y003_HAEIN	OMPB_RICCN	120K_RICRI	OMPB_RICRI	NUCL_HUMAN	FTSY_RICPR	WD21_HUMAN	YFC5_SHEFR	TPIS_AGRT5	PANB_OCEIH	YEIN_ECOLI	PUR6_CANAL	YT00_MYCTU	BCA1_MOUSE	BCA1_RAT	PBP_PLAFA	BRS3_MOUSE	ALP_CEPAC	OPS4_CANAL
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011178 caenorhabdi 005049 xenopus lae 064336 mus musculu 01650 homo sapien 016799 homo sapien 081511 methanosarc 015782 homo sapien 05241 human herpe 00475 brachydanio 092978 rickettsia 092cs7 rickettsia 092cs7 rickettsia
YPC1_CAEEL MUC1_XENLA TBR1_MOUSE TBR1_HUMAN RTN1_HUMAN RTN1_HUMAN GGSA_METAC C3L2_HUMAN UL49_HSV6U BLMG_BRARE RS13_RICCN RS13_RICCN RS13_RICCN
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ALIGNMENTS

RESULT 1

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PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE-20400020; Pubbed=10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pina L.A., Donella-Deana A.;
"Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine Kinases In intact human erythrocytes: identification of primary and secondary phosphorylation sites.",
Blood 96:1550-1557(2000).
                                                                                                                                                                                                                           MEDLINE-88228050; PubMed-3372523; Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki N.; "Localization of the pyridoxal phosphate binding site at the COOH-terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:822-8238(1988).
sequence, conformation and a possible molecular mechanism for anion exchange ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92107882; PubMed-1722314; Jacolim P., Sapak P., Nurse G.T., Rubin H.L., Zhai S., Sahr K.E., ilu S.-C.; Peletion in erythrocyte band 3 gene in malaria-resistant Southeast
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MEDLINE-92167271; PubMed=1538405;
Schoffeld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Okubo K., Hamasaki N., Hara K., Kageura M.;
"Palmitoylation of cysteine 69 from the COOH-terminal of band 3
protein in the human erythrocyte membrane. Acylation occurs in the
middle of the consensus sequence of F-I-IICLAVL found in band 3
protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
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Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney
Wajoman H., Bursaux E.,
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
characterization of the structural modification (Lys 56-->Glu) by
protein chemistry methods.";
Blood 78:1117-1120(1991).
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Jennings M.L., Smith J.S.;
Jennings M.L., Spirit J.S.;
Je
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MEDLINE-92329950; Pubmed-1378323;
Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basis of unique red cell membrane properties in hereditary
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MEDLINE-93343855; PubMed-8343110;
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J. Mol. Biol. 223:949-958(1992)
                                                                                                    Biochem. J. 213:577-586(1983).
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Gratzer W.B.;
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"Band 3 Tus
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VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of erythroid band 3 lead to a decrease in membrane-associated band 3 and to the phenotype of herealtary spherocytosis.";
                                                                                                                                                                                                      "Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";
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Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Allolaio N.;
Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of
transmembrane segment 11.";
                                                                                                                                                                                                                                                                                                         VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE=94266802; PubMed=8206915;
Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3; a site of interaction between band 3 and glycophorin A under certain conditions.";
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MEDLINE-96225450; PubMed-8640229;
EDER S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kudjer W., Oescan R., Pekun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
harkyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
Nat. Genet. 13:214-218(1996).
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Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozoi
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency.", Blood 88:4366-4374(1996).
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                                                                                                                                          MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.
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MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J.,
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                                                                                                                                                                                                                                                 cytoplasmic domain of band
Blood 81:2155-2165(1993).
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                                                                                                                        VARIANT MONTEFIORE
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID-10116;
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                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
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     Length 911;
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PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                            Indels
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TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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     Score 98; DB 1;
Pred. No. 1.5e-08;
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                                                            0; Mismatches
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IsoId=P23562-1; Sequence=Displayed;
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InterPro; IPR003020; HCO3_cotranspt.
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EMBL; L02943; AAA40801.1; -.
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J. Biol. Chem. 264:8185-8192(1989)
                                                                                                                                       731 SVTHANALTVMGKASTPGAA 750
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MEDLINE-89255254; PubMed-2722777;
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PRINTS: PR01231; HCO3TRNSPORT.
  100.0%;
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Query Match 100.
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Matches 20; Conservative
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P23562;
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Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion exchange protein."; Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
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                                                                                                                     POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
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                                                                                                                                                                                                                                                                                     1; Indels
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Koptico R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                      681A228474E5E9DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
          CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE).
                                                                                                          CYTOPLASMIC (POTENTIAL).
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Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Blochem. 29:1-17(1985).
                                                                                                                                                                                                                                                               Score 91; DB 1; I Pred. No. 2.2e-07;
 splicing
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Palmitate;
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P04919;
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September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
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101.679 Million cell updates/sec Run on:

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Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

*	Description	P02730 homo sapien	rattu	PO4919 mus musculu		rattus	mus mus	P48746 oryctolagus			mus n		P48751 homo sapien	018917 oryctolagus				Q63083 rattus norv	Q02818 homo sapien			O13923 schizosacch		~		m			~	-	1 lact	66		8 esche
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34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
 sequence, conformation and a possible molecular mechanism for anion
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WINDLINE-216721; PubMed-1538405;
Schoffeld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.
Nash G.B., Dizewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
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Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney, Wajcman H., Bursaux E.;
Wajcman H., Bursaux E.;
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characterization of the structural modification (Lys 56-->Glu) by
protein chemistry methods.";
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Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.
                                                                                      MEDLINE-88228050; PubMed-3372523; Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Localization of the pyridoxal phosphate binding site at terminal region of erythrocyte band 3 protein."; J. Biol. Chem. 263:8232-8238(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asian ovalocytosis.";
Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991).
                                                                                                                                                                                                          ROLE OF GLU-681, AND SEQUENCE OF 665-688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20400020; PubMed=10942405;
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MEDLINE-91358422; PubMed-1885574;
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                                     Biochem. J. 213:577-586(1983).
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MEDLINE-93343855; PubMed-8343110;

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WARÍANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-951349893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
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MEDLINE-96136073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.,
"Baklouti F., Tanner M.J., Delaunay J., Alloisio N.,
"Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Changes in the blood group Wright antigens are associated with a mutation at amino acid 658 in human erythrocyte band 3: a site of interaction between band 3 and glycophorin A under certain
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Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
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                                                                                                                                               MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
Schwartz R.S.;
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MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane segment 11.";
Br. J. Haematol. 91:804-810(1995).
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                                                                                     Biochem. J. 293:317-320(1993)
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Nat. Genet. 13:214-218(1996).
                                                                                                                             VARIANT MONTEFIORE LYS-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood 85:541-547(1995).
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Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-89255254; PubMed-2722777;
Kudrycki K.E., Shull G.E.;
Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
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         Ouery Match 100.0%; Score 96; DB 1; Length 911; Best Local Similarity 100.0%; Pred. No. 2.6e-07; Matches 20; Conservative 0; Mismatches 0; Indels
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SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=P23562-1; Sequence=Displayed;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS: PR01231; HCO3TRNSPORT.
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                                                                                                     Rattus norvegicus (Rat).
Bukaryota; Mertazoa; Chordata;
Mammalia; Butheria; Rodentia;
NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L02943; AAA40801.1; -. PIR; A33810; A33810.
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Kopito R.R., Lodish H.F.;
"Primary structure and transmembrane orientation of the murine anion
exchange protein.";
Nature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse),
bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                              13.AUG-1987 (Rel. 05, Created)
13.AUG-1987 (Rel. 05, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
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PALMITATE (BY SIMILARITY).
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                      MEMBRANE (ANION EXCHANGE)
                                                                                                                   CYTOPLASMIC (POTENTIAL).
splicing.
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Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
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MEDLINE-87250387; PubMed-3036795;
Kopito R.Y., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3
J. Biol. Chem. 262:8035-8040(1987).
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SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
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Best Local Similarity 95.0
Matches 19; Conservative
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 Palmitate;
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SLC4Al OR AE1.
Lipoprotein;
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· protein search, using sw model OM protein

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2; Search time 9.25 Seconds (without alignments) 101.679 Million cell updates/sec

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112 1 DRILLLFKPPKYHPDVPYVK 20 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

127863 seqs, 47026705 residues Searched:

hits satisfying chosen parameters: Total number of

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

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ALIGNMENTS

							Band 3 anion transport protein (Anion exchange protein 1) (AE 1)	,			brata; Euteleostomi;	Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo	
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LT 1	B3AT_HUMAN	B3AT_HUMAN	P02730;	21-JUL-198	01-APR-199	15-SEP-200	Band 3 ani	(CD233 antigen).	SLC4A1 OR	Homo sapiens (Human).	Eukaryota;	Mammalia;	NCBI TRATIONOS
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tomi; __TaxID=9606;

SEQUENCE FROM N.A.
MEDLINE-90083213; Pubwed-2594752;
Lux S.E., John K.M., Kopito R.R., Lodish H.F.;
"Cloning and characterization of band 3, the human erythrocyte anion-exchange protein (AEI).";
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Biochem. J. 256:703-712(1988). SEQUENCE OF 1-199; 220-292 AND 347-370. MEDLINE-90001294; PubMed-2790053;

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SEQUENCE OF 559-630.
MEDLINE-83308584; PubMed-6615451;
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sequence, conformation and a possible molecular mechanism for anion
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MEDLINE-92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis.";
                                                                             SEQUENCE OF 834-911.
MEDLINE-88228050; Pubmed-3372523;
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Kawano T., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki h
"Localization of the pytidoxal phosphate binding site at the COOH-
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protein in the human erythrocyte membrane. Acylation occurs in the middle of the consensus sequence of F-I-IICLAVL found in band 3
protein and G2 protein of Rift Valley fever virus.";
J. Blol. Chem. 266:16420-16424(1991).
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Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904 MEDLINE-20400020; Pubmed-10942405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 88:11022-11026(1991)
                                                                                                                                                                                                                         ROLE OF GLU-681, AND SEQUENCE OF 665-688.
MEDLINE-92332495; PubMed-1352774;
                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91358422; PubMed-1885574;
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MEDLINE-92167271; Pubmed-1538405;
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                                             Biochem. J. 213:577-586(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT MEMPHIS GLU-56
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Gratzer W.B.;
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VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE-95134893; PubMed=753050;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
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J. Biol. Chem. 269:16155-16158(1994).
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MEDLINE-96136073; PubMed=8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Allolsio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary
spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d with a site of
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MEDLINE-96225450; PubMed-8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kudjer W., Oescan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
Annyrin-I mutations are a major cause of dominant and recessive hereditary spherocytosis.";
Nat. Genet. 13:214-218(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tanner M.J., "Changes in the blood group Wright antigens are associated with mutation at amino acid 658 in human erythrocyte band 3: a site clinteraction between band 3 and glycophorin A under certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozo
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Characterization of 13 novel band 3 gene defects in hereditary spherocytosis with band 3 deficiency."; Blood 88:4366-4374(1996).
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Jarolim P., Murray J.L., Rubin H.L., Taylor W.M., Prchal J.T.,
Ballas S.K., Snyder L.M., Chrobak L., Melrose W.D., Brabec V.,
                                                                                                                       VARIANT MONTEFIORE LYS-40.
MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L., Schwartz R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT BLOOD GROUP WR(A).
MEDLINE-95111140; PubMed-7812009;
Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837
                                                                                                                                                                                                                                                                                                         VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE-94266802; PubMed-8206915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rransmembrane segment 11.";
3r. J. Haematol. 91:804-810(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANTS HS SER-147 AND MET-488.
MEDLINE-97351102; PubMed-9207478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conditions.";
Blood 85:541-547(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [23]
VARIANTS HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palek
                                                                                                                                                                                                                                                                                                                                                                                                                                                    18]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                   Rudrycki K.E., Shull G.E.;
Rudrycki K.E., Shull G.E.;
"Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SLC4Al OR AEI.
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     Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO(0834; ae; 1.
PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event-Alternative splicing; Named isoforms-2;
 100.0%; Score 112; DB 1;
100.0%; Pred. No. 3.2e-09;
ive 0; Mismatches 0;
                                                                                                                                                             927 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name-Kidney;
IsoId-P23562-2; Sequence-VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId-P23562-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A3381v, no. 1876.
HSSP; P02730, 1BTG.
InterPro; IPR003717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00055; HC03_cotranspt.
Pfam; PF00153; HC03_cotranspt.
                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04793; AAA40800.1; ALT_INIT.
EMBL; L02943; AAA40801.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989)
                                                                          DRILLLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                                               TISSUE-Kidney;
MEDLINE-89255254; PubMed-2722777;
                                                         1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-45 FROM N.A.
Ouery Match
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COLLECTING DUCTS.
                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10116;
                                                                                      807
                                                                                                                               RESULT 2
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[1] SEQUENCE FROM N.A. MEDLINE-85568011; Pubmed=2410791; Kopito R.R., Lodish H.F.; cansmembrane orientation of the murine anion "Primary Structure and transmembrane orientation of the murine anion exchange protein."; Mature 316:234-238(1985).
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota: Metazoa, Chordata, Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
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0
                                                                                                                                                                                                                                                                           Length 927;
                                                                                         EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                               Score 108; DB 1; Length %2 Pred. No. 1.3e-08;
                                                                                                                                     EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87250387; PubMed-3036795; Kopito R.R., Andersson M., Loddish H.F.; "Structure and organization of the murine band 3 gene."; J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kopito R.R.;
Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases
native splicing.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                         rid=vsp_000455.
681A228474E5E9DE CRC64;
                                                                                                              CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDAMEd-3840489; MEDLINE-86034211; PubAmed-3840489; MEDLINE-86034211; PubAmed-3840489; Structure of the murine anion exchange protein."; Structure of the murine anion oxchange protein."; J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                        929 AA
                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                              POTENTIAL.
                                                                                                     POTENTIAL.
                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                     [5]
SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
                                                                                                                                                                                                                                                                                                                         1 DRILLERPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                     103172 MW;
                                                                                                                                                                                                                                                                           96.4%;
95.0%;
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
 Palmitate;
                                                                                                                                    676
696
735
735
736
822
881
658
859
79
                                                                                                                                                                                                                                                   927 AA;
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                                                                5508
5508
5509
505
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SLC4A1 OR AE1.
 Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                     B3AT_MOUSE
P04919;
                     DOMAIN
TRANSMEM
TRANSMEM
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TRANSMEM
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                     FRANSMEM
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                                                                                         DOMAIN
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                                                                                                                                                                                                                                                             -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-1- SUBCELLUIAR LOCATION: Integral membrane protein.
-1- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                     Passow H.; "Major proteclytic fragments of the murine band 3 protein as obtained
                                                                                                                                                                                                 Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
POTENTIAL.
N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXOPLASMIC LOOP (POTENTIAL).
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POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOId=P04919-2; Sequence=VSP_000454;
-1- TISSUE SPECIFICITY: ERYTHROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (PÓTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms-2;
                                                                                                                        [6]
SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed-2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, X02677; CAA26506.1; -... EMBL, M29379; AAA37187.1; -... EMBL, J02756; AAA37278.1; -... EMBL, X03917; CAA27555.1; -... PIR, A25314; A25314; A25314; A25314; A25314; A25314; A25314; A25319; IBTS. MGD: MGI: 109393; Slc4al. InterPro; IPR001717; Anion_exchange. InterPro; IPR003020; HCO3_cotranspt. Pfam; PP00955; HCO3_cotranspt.
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                                                                             band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGREAMS; TIGRO0834; ae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name-Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipoprotein;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM'N.A.
MEDLINE-89039870; PubMed-3185555;
Kim H.R.C., Yew N.S., Ansorge W., Voss H., Schwager C.,
Vennstroom B., Zenke M., Engel J.D.;
Two different mRNas are transcribed from a single genomic locus encoding the chicken erythrocyte anion transport proteins (band 3).";
Mol. Cell. Biol. 8:4416-4424(1988).
-I- FUNCTION: BAND 3 IS THE MADON INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAIN S. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROS INTEGRAL DOMAIN MERRAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: ENTITROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                          ô
                                                                                                                                                                          Length 929;
                                                                                                                                              Score 108; DB 1; Lengtn >2.
Pred. No. 1.3e-08;
                              79 Missing (in isoform Kidney).
/FIGAVSp_000454.
67 G -> S (IN REF. 5).
103135 MW; 5C0E281C394FB614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00210; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
DOMAIN 1 416 CYTOPLASMIC (POTENTIAL).
DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).
   PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           922 AA
                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
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InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                              825 DRILLEKPPKYHPDVPFVK 844
                                                                                                                                                                                                                                                                                            1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00955; HCO3 cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGRO0834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Band 3 anion transport protein. Gallus gallus (Chicken)
                                                                                                                                                                             96.4%;
95.0%;
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                                                                                                                                                                                                        1 Similarity 95.0 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                               929 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B3AT_CHICK
P15575;
LIPID
VARSPLIC
                                                                                                               SEQUENCE
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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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protein search, using sw model protein ŏ

3, 2003, 11:41:03 September Run on:

33 ; Search time 17.25 Seconds
(without alignments)
111.500 Million cell updates/sec

US-10-087-464-1

1 GMPWLSATTVRSVTHANALT 20 score: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283308 segs, 96168682 residues hed:

seq length: 0 seq length: 2000000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
п	104	100.0	848	!	A33810	band 3 anion tran
2	104	100.0	911		взно	band 3 anion tran
3	104	100.0	929		A25314	m
4	100	96.2	844	Ġ	I50159	+
2	100	96.2	922		A30816	band 3 anion tran
9	95	91.3	912		S59861	e
7	95	91.3	918		S24318	band 3 anion tran
8	93	89.4	865		A25104	band 3 protein, n
6	93	89.4			A34911	band 3-related pr
10	93	Φ			A31789	3-related
11	93	89.4			A56764	
12	93	89.4			S21086	anion exchange pr
13	89	85.6			A42497	-
14	88	85.6			B34911	band 3-related pr
15	88				A33638	erythrocyte anion
16	88		1232		I38496	anion exchanger 3
17	84		357		S31828	band 3 anion tran
18	53		826		T28858	hypothetical prot
19	48	46.2	314		T44895	probable lipoic a
20	47	45.2	1035		T31336	sodium bicarbonat
21	47		1035		T13962	sodium bicarbonat
22	47	•	1035		T14110	sodium bicarbonat
23	47	•	1079		PC7034	Na+ bicarbonate c
24	47		1079		T14031	sodium bicarbonat
25	46	44.2	156		C72506	hypothetical prot
56	45		111		B72722	
. 27	45	43.3	302		F69000	
28	45	43.3	727	7	68	·
29	45	43.3	1119	7	T37460	probable sodium b

hypothetical prote probable cytochrom hypothetical prote hypothetical prote NADH2 dehydrogenas hypothetical prote probable lipoic ac hypothetical prote probable lipoic ac hypothetical prote PHO85-like protein	u-plasminogen acti cytochrome c-type hypothetical prote cytochrome c-type iron binding prote hypothetical prote glycine betaine/L-
T22491 H70526 T27828 T11840 D83699 C70787 T422841	UKHU E57987 D86101 H91260 T45065 D83563 MMECPW
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## ALIGNMENTS

transport protein - rat band 3 anion

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Caccession: A33810
C;Accession: A33810
B;Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr A;Reference number: A33810; MUID:89255254; PMID:2722777
A;Accession: A33810

A;Status: preliminary

A; Molecule, type: mRNA A; Residues: 1-848 -KUD. A; Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093 C; Superfamily: band 3 anion transport protein C; Keywords: alternative splicing; transmembrane protein

Length.848;

Gaps ö Indels Score 104; DB 2; Pred. No. 8.3e-09; Mismatches ; 0 100.0%; Query Match 100. Best Local Similarity 100. Matches 20; Conservative

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1 GMPWLSATTVRSVTHANALT 20

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GMPWLSATTVRSVTHANALT 676 g

RESULT 2

band 3 anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #405237; A26507; A92430; A90323; A28079; R;Lux, S.E.; John, K.M.; Kopito, R.R.; L9409; A92237; A26507; A92430; A90323; A28079; Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989
A;Title: Clonling and characterization of band 3, the human erythrocyte anion-exchange A;Reference number: A36218; MUID:90083213; PMID:2594752

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-911 <LUX>

A;Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
R;Tanner, M.J.A.; Martin, P.G.; High, S.
Blochem. J. 256, 703-712, 1986
A;Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra
A;Reference number: S03074; MUID:89134172; PMID:3223947

A;Molecule type: mRNA A;Residues: 1-55,7E,7E,75-911 <TAN> A;Cross-references: EMBL:X12609; NID:928713; PIDN:CAA31128.1; PID:928714 R;Showe, L.C.; Ballantine, M.; Huebner, K.

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A;Note: sequence extracted from NUBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:1138 A;Note: a histidine residue essential for anion transport is suggested to be His-651, R;Okubo, K; Kang, D; Hamsaski, N; Jennings, M.L.
J. Biol. Chem. 269, 1194-1926, 1994
A.Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS A;Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Rolecule type: protein
A; Rolecule type: 436,479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A; Role: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transpo
B; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Blochem. 122, 577-585, 1997
A; Title: Proteoilytic cleavage sites of band 3 protein in alkali-treated membranes: Fi
A; Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm 1-403/Region: cytoskeletal protein binding
                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826
A;Experimental source: erythrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                        J. Biol. Chem. 267, 19211-19217, 1992
A; Title: A structural study of the membrane domain of band 3 by tryptic digestion.
A; Reference number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                              Kuroda, N.; Shiraki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status predicted <TM06>
transmembrane #status predicted <TM07>
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transmembrane #status predicted <TM10>
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Modified site: acetylated amino end (Met) #status ex
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map position: 17q21-17q22 Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: GDB:SLC4A1; BPB3
A; Cross-references: GDB:119874; OMIN:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transmembrane #status
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em. 267, 19211-19217, 1992
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Best Local Similarity
Local 20; Conserve
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A; Residues: 559 630 <BRO>
A; Note: Lys-590 was shown to bind phenyl isothiccyanate, an inhibitor of anion transport
B; Kawano, Y; Okubo, K; Tokunaga, F; Miyata, T; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A; Reference number: A28079; MUID:88228050; PMID:3372523
Genomics 1, 71-76, 1987
A:Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPH A:Reference number: 139408; MUID:88031311; PMID:3478298
                                                                                                                                                                                                                                                                                        A, Molecule type: DNA
A, Residues: 118-161 <SHO2>
A, Crost-reneces: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169
R; Drickamer, L.K.
J. Biol. Chem. 253, 7242-7248, 1978
A; Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Identif
A; Reference number: A92237; MUID:79027186; PMID:701248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
Residues: 1-3 < DRI>
Residues: 1-3 < CRI>
awby, W.J.; Findlay, J.B.C.
chem. J. 205, 465-475, 1982
A; Title: Characterization and partial sequence of di-lodosulphophenyl isothiocyanate-bin A; Reference number: A26507; MUID:83074521; PMID:7150226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: protein
A; Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 < YANI>
R; Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8283-8290, 1990
A; Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human erythrocyte
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Residues: 834-842, XX, 844-911 < KAW>
Residues: 834-842, XX, 844-911 < KAW>
Residues: 834-845, XX, 844-911 < KAW>
Residues: 834-845, Washown to blud the affinity label pyridoxal phosphate, a substrate fixannoukakos, D.; Vasseur, C.; Bluquilt, Y.; Bursaux, E.; Wajcman, H.
Biochim. Biophys. Acta 998, 43-49, 1989
A.Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band A; Reference number: S05523; MUID:90001294; PMID:2790053
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A;Molecule type: protein
A;Molecule type: protein
A;Rolecule type: protein
A;Rolecule 1364, X', 366-372;424-429, 'X', 431-434 <COB>
A;Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B;Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, X.; Delaunay, J.; Wajcman, Blood 78, 1117-1120, 1991
                                                                                                                                    A;Molecule type: DNA
A;Realdues: 37-56 <SHO1>
A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A;Accession: 139409
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A,Residues: 437-473;360-364,'D',366-369 <MAW>
R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
J. Biol. Chem. 258; 7981-7990, 1983
A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of A;Reference number: A92430; MUID:83238395; PMID:6345535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: The human erythrocyte anion-transport protein. A;Reference number: A90323; MUID:83308584; PMID:6615451 A;Accession: A90323
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A;Residues: 1-10, D; 12-68, E', 69-200 <KAU>
R;Brock, C.J.; Tanner, M.J.A.; Kempf, C.
Blochem. J. 213, 577-586, 1983
                                                                                                                     Accession: I39408
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A; Reference A; Accessio

A25314

Dand 3 protein - mouse

Dand 3 protein - mouse

Dand 3 protein - mouse

C; Species: Max musculus (house mouse)

C; Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999

C; Accession: A25314; A26086; I49524; B25104

R; Kopito, R. R.; Lodish, H.F.

Nature 316, 234-238, 1985

A; Title: Primary structure and transmembrane orientation of the murine anion exchange

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C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revi
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R; Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A; Title: Alternative primary structures in the transmembrane domain of the chicken eryth A; Reference number: I50159; MUD: 88216609; PMID: 2835670
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A; Residues: 4-707, 'x', 709-902 <RES>
A; Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
R; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera
EMBO J. 5, 1205-1214, 1986
A; Title: Clouing and structural characterization of a human non-erythroid band 3-like pr
A; Reference number: A91039; MUID:86274622; PMID:3015590
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C;Keywords: transmembrane protein
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C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
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C;Superfamily: band 3 anion transport protein
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A; Residues: 1-929 < KRO2>
A; Cross-references: GB: MX29379; NID:g191741; PIDN:AAA37187.1; PID:g191742

A; Cross-references: GB: MX29379; NID:g191741; PIDN:AAA37187.1; PID:g191742

R; Kopito, R. R; Andersson, M.; Lodish, H. F.

G. Biol. Chem. 262, 8035-8040, 1987

A; Title: Structure and organization of the murine band 3 gene.

A; Reference number: 149524; MUID:87250387; PMID:3036795
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A; Residues: 11-466,'S',468-929 <DEM>
A; Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C; Genetics:
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A; Residues: 1-929 <KOP>
A; Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
A; Kopito, R.R.; Lodish, H.F.
T. Cell: Blochem. 29, 1-17, 1985
A; Tille: Structure 20, the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
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Pred. No. 9.2e-09;
Mismatches 0;
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Pred. No. 3.7e-08;
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Status: preliminary: translated from GB/EMBL/DDBJ
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band 3 anion transport protein (clone pBIIIC1)
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Best Local Similarity 100.0%; P:
Matches 20; Conservative 0;
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les 18; Conserv
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A; Accession: A. Regidners: I-regidners: I-regidners: I-regidners: I-regidners: I-regidners: Beginners: Beginn
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R;Fievet, B.; Gabillat, N.; Borgese, F.; Wotais, R.
EMBO J. 14, 5158-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Reference number: S59861; MUID:96080151; PMID:7489705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Oncorhynchus mykiss (rainbow trout)
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Species: Oncorhynchus mykiss (rainbow trout)
C; Date: 07-Apr-1994 #text_change 20-Aug-1999
C; Date: 07-Apr-1994 #text_change 20-Aug-1999
C; Accession: S; Aichel, F: Rudloff, V.; Appelhans, H.
BiOchem. J. 285, 17-23, 1992
BiOchem. J. 285, 17-23, 1992
A; Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive A; Reference number: S24318; MUID:92344566; PMID:1637296
     C; Accession: A30816
R; Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A; Title: Two different mRNAs are transcribed from a single genomic locus encoding the A; Reference number: A30816; MuID: 89039870; PMID:3185555
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C,Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
#sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
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A;Cross-references: EMBL:X61699; NID:964308; PIDN:CAA43868.1; PID:964309
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Pred. No. 4.1e-08;
2; Mismatches 0;
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Pred. No. 2.7e-07;
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A;Reference number: S22173
A;Accession: S22173
                                                                                                                                                                                                                                     A; Residues: 1-922 <KIM>A; Cross-references: GB:M23404
C; Superfamily: band 3 anion transport protein
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A;Accession: S36083
A;Molecule type: protein
A;Residues: 71-89;94-114;570-588 <HUE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                731 GMPWLSATTVRTITHANALT 750
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Best Local Similarity 90.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                            96.2%;
ilarity 90.0%;
Conservative
                                                                                                                                                                                                                                                                                                                             C; Keywords: transmembrane protein
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A; Residues: 1-918 <HUEl>
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A; Residues: 1-912 <FIE>
                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 18; Conserv
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                                                                                                                                                                                                                A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S59861
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    chicken
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protein search, using sw model OM protein 3; Search time 17.25 Seconds (without alignments) 111.500 Million cell updates/sec 3, 2003, 11:41:03 September Run on:

1 SVTHANALTVMGKASTPGAA 20 US-10-087-464-2 98 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283308 seqs, 96168682 residues Searched:

number of hits satisfying chosen parameters:

283308

seq length: 0 seq length: 2000000000 8 1 1 1 1 1 Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_76:*
1: pirl:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

band 3 anion trans band 3 anion trans Description SUMMARIES Ωī - 0 DB Query Match Length 100.0 Score 98 Š. Result

, (	s process	band 3 protein, no	band 3-related pro	band 3-related pro		anion exchange pro	anion transporter	band 3 anion trans	band 3 anion trans	band 3 anion trans	anion exchanger 3,	band 3-related pro	erythrocyte anion	anion exchanger 3	band 3 anion trans		hypothetical prote	н	outer membrane pro	proline dehydrogen	transferase homolo	nucleolin - human	cell division prot	probable transcrip	basic leucine zipp	hypothetical prote	_
7	A23314	A25104	A34911	A31789	A56764	S21086	I50159	A30816	S59861	S24318	A42497	B34911	A33638	I38496	S31828	I64139	E97835	н95911	S07575	T28435	T30585	A35804	B71638	E95911	T09120	T19835	T47801
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	7	74	74	74	74	74	72	72	64	64	62	62	62	62	58	20	4	48	48	45	44	43	42	42	4	4	42
15	7	73	73	73	73	73	71	71	63	63	61	61	.61	61	57	49	48	47.5	47	45	44	42.5	42	42	42	45	42
1 (	7	4	2	9	_	œ	σ	10	:	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	78	58

polyketide synthas hypothetical prote	orf1 5' to fcc - S triosephosphate is	triosephosphate is geranylgeranyl dip	ABC transporter, s	probable solute-bi	probable nucleic a	probable RTX famil	hypothetical prote	latent transformin	translation initia	hypothetical prote	hypothetical prote	methionine aminope
T17409 T12541	A44238 AH2775	F97555 C75400	AG2724	C97506	H75272	B85547	F90696	A55494	AE3544	A82459	T37094	B87106
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42.9	41.8	41.8	41.8	41.8	41.8	41.8	41.8	41.3	40.8	40.8	40.8	40.8
42	41	4141	41	41	41	41	41	40.5	40	40	40	40
30 31	33	34	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

Danid 3 anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchanger, species: Homo Sapiens (man) (5;Species: Homo Sapiens (man) (6;Date: 03-aug-1984 #sequence_revision 03-oct-1995 #text_change 22-Jun-1999 (5;Date: 03-aug-1984 #sequence_revision 03-oct-1995 #text_change 22-Jun-1999 (5;Date: 03-aug-1984 #sequence_revision (03-oct-1995 #text_change 22-Jun-1999 (5;Date: 03-aug-1984 #sequence] R;Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F. Proc. Natl. Acad. Sci. Us.A. 86, 9089-9093, 1989 #the human erythrocyte anion-exchange A;Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange A;Accession: A36218

A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-911 <LUX>
A; Molecule type: mRNA
A; Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
B; Tanner, M.J.A.; Martin, P.G.; High, S.
Biochem J. 256, 703-712, 1988
A; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr
A; Reference number: S03074; MUID:89134172; PMID:3223947

A; Accession: \$03074
A; Molecule type: mRNA
A; Residues: 1-55. Er, 57-911 <TAN>
A; Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714
A; Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714
B; Showe, L.C.; Ballantine, M.; Huebner, K.
Genomics 1, 71-76, 1987
A; Title: Localization of the gene for the erythroid anion exchange protein, band 3 (A; Reference number: 139408; MUID:88031311; PMID:3478298
A; Accession: 139408

A;Molecule type: DNA A;ResIduse: 37-56 <SHO1> A;Crost references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220 A;Accession: 139409

A;Molecule type: DNA A;Residues: 118-161 <SHO2> A;Cross-references: GB:M16979; NID:9178218; PIDN:AAA51671.1; PID:9553169

R;Drickamer, L.K. J. Biol. Chem. 253, 7242-7248, 1978 A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide A;Reference number: A92237; MUID:79027186; PMID:701248

A,Molecule type: protein A,Residues: 1-3 <DRI> R,Mawby, W.J.; Findlay, J.B.C. Biochem. J. 205, 465-475, 1982 A,7tile: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate A,Reference number: A26507; MUID:83074521; PMID:7150226

Ξ A;Molecule type: protein A;Residues: 437-473;360-364,'D',366-369 <WAW> R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, J. Blol. Chem. 258, 7981-7990, 1983

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domain mediates a

omains. Its integral doma enzymes, and hemoglobin.

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A33810

Dand 3 anion transport protein - rat

C.Species: Rattus norvegicus (Norway rat)

C.Accession: A33810

R.Kudrycki, K.E.; Shull, G.E.

J. Biol. Chem. 264, 8185-8192, 1989

A.Tille: Primary structure of the rat kidney band 3 anion exchange protein deduced fracession: A33810; MulD:89255254; PMID:2722777

A.Accession: A33810; MulD:89255254; PMID:2722777

A.Status: preliminary

A.Status: preliminary

A.Residucs: 1-848 < KUD>

A.Residucs: 1-848 < KUD>

C.Superfamily: band 3 anion transport protein

C.Superfamily: band 3 anion transmembrane protein

C.Superfamily: band 3 anion transmembrane protein
                                                                                                                                                                                                                    A/Map position: 17421-17422
Cisuperfamily: band 3 anion transport protein
Cisuperfamily: band 3 anion transport protein
Cisuperfamily: band 3 anion transport protein; ion transport; phosphoprotein; transm
Cisty votas ectylated amino end; glycoprotein; ion transport; phosphoprotein; transm
F;404-911/Region: cytoskeletal protein binding
F;404-617/Romain: transmembrane #status predicted <TMO1>
F;455-457/Domain: transmembrane #status predicted <TMO3>
F;459-479/Domain: transmembrane #status predicted <TMO4>
F;581-547/Domain: transmembrane #status predicted <TMO5>
F;688-588/Domain: transmembrane #status predicted <TMO6>
F;604-624/Domain: transmembrane #status predicted <TMO6>
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C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A55314; A56086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;642/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Met) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F:1/Modified site: acetylated amino end (Met) #status experi
F:559,590,851/Binding site: anion (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;861-881/Domain: transmembrane #status predicted <TM14>
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95.0%; Pred. No. 6.7e-07;
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F;785-806/Domain: transmembrane #status predicted
F;839-859/Domain: transmembrane #status predicted
                                               Comment: Band 3 has at least two functional do
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              731 SVTHANALTVMGKASTPGAA 750
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20; Conservative (
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Best Local Similarity 95.0°
Matches 19; Conservative
                                                                                                                                                         A; Gene: GDB:SLC4A1; EPB3
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                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 559-630 <a href="Mailto: Lys-590">Mailto: Lys-590</a> was shown to bind phenyl isothiocyanate, an inhibitor of anion transport R; Kawano, Y; Okubo, K; Tokunaga, F; Miyata, T; Iwanaga, S; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic A; Reference number: A28079; MUID:88228050; PMID:3372523
A;Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A;Reference number: A92430; MUD:83238395; PMID:6345535
A;Accession: A92430
A;Ablecule type: protein
A;Residues: 1-10, 'D',12-68,'E',69-200 <KAU>
B;Brock, C.J; Tanner, M.J.A.; Kempf, C.
Biochem. J. 213, 577-586, 1983
A;Title: The human erythrocyte anion-transport protein.
A;Reference number: A90323; MUD:83308584; PMID:6615451
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A; Residues: 361-364, X', 366-372; 424-429, 'X', 431-434 <COB>
A; Residues: 361-364, X', 366-372; 424-429, 'X', 431-434 <COB>
A; Note: Lys-430 is labeled by eosiny1-5-maleimide (EMA) in intact erythrocytes
R; Yannoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 1-55, E', 57-69 < YAN2>
A; Residues: 1-55, E', 57-69 < YAN2>
A; Note: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; Chem. 267, 19211-19217, 1992
A; Test a structural study of the membrane domain of band 3 by tryptic digestion. Confc A; Accession: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 78, 1117-1120, 1991
A:Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the
A:Reference number: A44933; MUID:91329825; PMID:1678289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Accession: A28079
A. Culle type: protein
A. Culle type: protein
A. Culle type: protein
A. Culle: 834-842, x', 844-911 <KAW>
A. Culles: 834-851 was shown to bind the affinity label pyridoxal phosphate, a substrate for the grannow that shown to bind the affinity label pyridoxal phosphate, a substrate for the protein Blophys. Acta 988, 43-49, 1989
A. Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band A; Reference number: 805523; MuID:90001294; PMID:2790053
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Residues: 361-911 <HAM>
Resent: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
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A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport
R;Hamasaki, N; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
T Riochem. 122, 577-585, 1997
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J. Bitle: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
A;Reference number: PC4403; MUID:98006310; PMID:9348087
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A; Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <K.
A; Experimental source: erythrocyte
A; Experimental source: erythrocyte
A; Note: sequence extracted from NCB1 backbone (NCBIP:113819, NCBIP:113821, NCBIP:11382
A; Note: a histidine residue essential for anion transport is suggested to be His-651, 1
B; Okubo, K.; Kang, D.; Hamasakl, N.; Jennings, M.L.
A; Eltle: Red biod cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS
A; Reference number: A49717; MUID:94124538; PMID:8294441
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Gaps

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DB 1;

<TM07> <TM09> <TM11><TM12>

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Indels

Length 848;

A;Reference number: A25314; MUID:85268011; PMID:2410791 A;Accession: A25314

Status: preliminary; translated from GB/EMBL/DDBJ

A; Accession: B25104

Molecule type: mRNA

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A;Title: Functional expression and subcellular localization of an anion exchanger A;Recence number: A35770; MUID:90319095; PMID:2371270
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual standard mRNA
A;Residues: 1-205, A/, 207-924, PG', 927-1017, 'IV', 1020-1155, 'ID', 1158-1234 <LIN>C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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(Species: Mus musculus (house mouse)
(Species: Mus musculus (house mouse)
(Spate: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
(Spacession: A1789
R;Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
A; Biol. Chem. 263, 17092-17099, 1988
A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney
A;Reference number: A31789; MUID:89034212; PMID:3182834
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A3570
C;Accession: A34911; A3570
B;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
J. Biol. Chem. 265, 462-471, 1990
A;Title: DNA cloning and tissue distribution of mRNAs for two proteins that are a A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1; PID:9203091
Lee, B.S.; Kopito, R.R.
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A; Residues: 1-127 <ALP>
A; Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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A;Molecule type: mRNA
A;Residues: 1-1234 < KUD>
A;Residues: 1-1234 < KUD>
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1;
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Pred. No. 0.00099;
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Pred. No. 0.00099;
0; Mismatches 3.
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3%;
Matches 15; Conservative
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A;Molecule type: mRNA
A;Residues: 1-1237 <CHO>
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Desidues: 4-707, X, 709-902 <RES>
Desidues: 4-707, X, 709-902 <RES

Desidues: 4-707, X, 709-902 <RES

Desidues: 4-707, X, 709-902 <RES

Desidues: A, 710-6-701, Res

Desidues: A, 700-701, Res

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
Cession: A25104
EMBO J. 5. 1205-1214, 1986
A;Title: Cloining and structural characterization of a human non-erythroid band 3-like pr A;Reference number: A91039; MUID:86274622; PMID:3015590
A;Accession: A25104
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C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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A; Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kopito, R.R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 252, 8035-8040, 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: I49524; MUID:87250387; PMID:3036795
A; Accession: I49524
                                                                    A; Molecule type: mRNA
A; Residues: 1-929 < KOP>
A; Cross-references: GB: CAD1677; NID: g49897; PIDN: CAA26506.1; PID: g49898
A; Cross-references: GB: CAD18, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID: 86034211; PMID: 3840489
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A; Residues: 11-466,'S',468-929 <DEM>
A; Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C; Genetics:
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A; Residues: 1-865 <DEM>
A; Cross-references: GB:N>
A; Cross-references: GB:N>
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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Pred. No. 7.4e-07;
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Pred. No. 0.00068;
Mismatches 3; Indels
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1 SVTHANALTVMGKASTPGAA 20

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74.5%;

Query Match
Best Local Similarity 83.33
Matches 15; Conservative

SVTHANALIVMGKASTPG 18

ð 셤 A34911 band 3-related protein 2

RESULT 5

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Query Match 92.9%; Best Local Similarity 95.0%; Matches 19; Conservative 0

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

3, 2003, 11:41:03 ; Search time 17.25 Seconds (without alignments) 111.500 Million cell updates/sec September : oo

GKASTPGAAAQIQEVKEQRI 20 US-10-087-464-3 96 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283308 seqs, 96168682 residues Searched:

I number of hits satisfying chosen parameters: DB seq length: 0 DB seq length: 2000000000 Maximum ET III

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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æ	Query	100.0	92.7	92.7	63.5	63.5	60.4	60.4	60.4	60.4	60.4		56.2	56.2	56.2	56.2	52.1	50.0		46.9	46.9	46.9	46.9	45.8	45.8	45.8	45.8	45.8	44.8	
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786 937 258	936 305 961	141 160 191	984 597 547	338
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# ALIGNMENTS

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transport protein, erythrocyte - numau
names: carrier family 4, anion exchanger, member 1; erythroid anion exc) band

A;MOlecule type: DNA A;Residues: 37-56 <SHO1> A;Cross.references: GB:M16978; NID:9178217; PIDN:AAA51670.1; PID:9178220

A; Accession: I39409

A; Modecule type: DNA A; Residues: 118-161 <SHO2> A;Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169 R;Drickamer, L.K. J. Biol. Chem. 253; 7242-7248, 1978 A;Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide A;Reference number: A92237; MUID:79027186; PMID:701248

A.Molecule type: protein
A.Residues: 1-3 <DRI>
R.Mawby, W.J.; Findlay, J.B.C.
B.Occhem. J. 205, 465-475, 1982
A.Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate
A.Reference number: A26507; WID:83074521; PMID:7150226
A.Rocession: A26507; WID:83074521; PMID:7150226
A.Rocession: A26507
A.Molecule type: protein
A.Residues: 437-473;360-364, 'D', 366-369 <MAW>
R.Residues: 437-473;360-364, 'D', 266-369 <MAW>
B.Residues: 437-473;360-364, 'D', 1983
J. Biol. Chem. 258, 7981-7990, 1983

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C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A55314, A56086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                              ion transport; phosphoprotein; transm
              two functional domains. Its integral domain mediates
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R;Kudrycki, K.E.; Shull, G.E.
J. Blol. Chem. 264, 8185-8192, 1989
A;Tille: Primary structure of the rat kidney band 3 anion exchange protein deduced A;Reference number: A33810; MUID:89255254; PMID:2722777
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C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
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A. Residues: 1-848 <KUD>
A. Cross-references: GB-104793; NID:g203092; PIDN:AAA40800.1; PID:g203093
C. Superfamily: band 3 anion transport protein
C. Keywords: alternative splicing; transmembrane protein
                                                    sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
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Pred. No. 1.2e-05;
0; Mismatches 1; Indels
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<TM10>
<TM11>
<TM12>
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1.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane #status predicted <I
                                                                                                                                                                                                                     A Map position: 17q21-17q22
C; Superfamily: band 3 anion transport protein
C; Superfamily: band 3 anion transport protein
C; Superfamily: band 3 anion transport protein
C; Superfamily: band 3 anion transport protein; ion
C; Keywords: acetylated amino end; glycoprotein; ion
C; Keywords: acetylated amino end; glycoprotein; ion
E; 1409-37Region: cytoskeletal protein binding
E; 405-427/Bomain: transmembrane #status predicted
E; 435-477/Bomain: transmembrane #status predicted
E; 459-479/Bomain: transmembrane #status predicted
E; 568-588/Bomain: transmembrane #status predicted
E; 568-588/Bomain: transmembrane #status predicted
E; 701-721/Bomain: transmembrane #status
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transmembrane #status predicted
transmembrane #status predicted
transmembrane #status predicted
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                                                                                                                                         A)Gene: GDB:SLC4A1; EPB3
A;Cross-references: GDB:119874; OMIM:109270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /Domain: transmembrane #status
led site: acetylated amino end
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.7%;
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nes 20; Conservative
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Matches 19, Conserv
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A25314
band 3 protein - mouse
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A; Status: preliminary
A; Molecule type: mRNA
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Matches
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A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regid A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regid A; Fesidues: 834-842, 74, 844-911 cKAW>
A; Fesidues: 834-842, 74, 844-911 cKAW>
A; Fesidues: 834-842, 74, 844-911 cKAW>
A; Residues: 834-842, 74, 844-911 cKAW>
A; Residues: 834-851 was shown to bind the affinity label pyridoxal phosphate, a substrate fc R; Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.
Biochim: Biophys: Acta 998, 43-49, 1989
A; Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3 A; Reference number: S05523; MUID:90001294; PMID:2790053
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C:Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
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A; Residues: 361-372; 390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 < KAN
A; Residues: 361-372; 390-399; 604-613; 632-639; 647-656; 699-729; 731-743; 761-781; 818-826 < KAN
A; Residues: 361-372; 390-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 810-82; 
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A; Residues: 1-201;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 < YAN1>
R; Cobb, C.E.; Beth, A.H.
Bjochemistry 29, 8283-8290, 1990
A; Title: Identification of the eosiny1-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
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A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A;Note: Lys-539 and Lys-531 were shown to bind the same molecule of the anion transport
R;Hamasaki, N; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Blochem. 122, 577-585, 1997
A;Title: Amino acid sequence of the N(alpha)·terminal 201 residues of human erythrocyte A;Reference number: A92430; MUID:83238395; PMID:6345535 A;Accession: A92430 A;Accession: A92430 A;Molecule type: protein
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A; Reference number: PC4403; MUID:98006310; PMID:9348087
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A; Residues: 1-10, D',12-68, E',69-200 <KAU>
R; Brochen, J. 213, 577-586, 1983
A; Title: The human erythrocyte anion-transport protein.
A; Reference number: A90323; MUID:83308584; PMID:6615451
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A; Molecule type: protein
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Gaps

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C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
C;Accession: A30816
B;Kiw, H;R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, R;Kiw, H;R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Title: Two different mRNAs are transcribe; MUID:89039870; PMID:3185555
A;Accession: A30816
A;Molecule type: mRNA
A;Residues: 1-922 <RNA>
A;Gcross-references: GB:M23404
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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band 3 protein, nonerythroid (MEB3) - human (fragment)

band 3 protein, nonerythroid (MEB3) - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999

C; Accession: A25104

C; Accession: A25104

EMBO J. 5, 1205-1214, 1986

A; Title: Cloning and structural characterization of a human non-erythroid band 3-like

A; Reference number: A91039; MUID:86274622; PMID:3015590
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911, A35770
Biol. Chem. 265, 462-471, 1990
R;KudryCki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
R;KudryCki, K.E.; Newman, P.R.; Shull, G.E.
A;Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are relf.
A;Accession: A34911
A;Feference number: A34911
A;Accession: A34911
A;Accession: A74011
A;Accession: A34911
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A;Title: Functional expression and subcellular localization of an anion exchanger cl.
A;Reference number: A35770
A;Accession: 
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A; Residues: 1-865 <DEM>
A; Residues: 1-865 <DEM>
A; Cross-references: GB:X03918; NID:g32120; PIDN:CAA27556.1; PID:g32121
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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0.27;
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Pred. No. (
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Pred. No. (
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R;Cox, J.V.; Lazarides, E. Moll. Cell. Biol. 8, 1327-1335, 1988
A,Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID:88216609; PMID:2835670
A;Accession: 150159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 4-707, 'X', '709-902 <RES>
A;Cross-references: GB:002756; NID:g192136; PIDN:AAA37278.1; PID:g553874
A;Cross-references: GB:002756; NID:g192136; PIDN:AAA37278.1; PID:g553874
B;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovera
EMBO J. S, 1206-1214, 1986
A;Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A;Reference number: A91039; MuID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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                                                                                          A; Molecule type: mRNA
A; Residues: 1-929 < KKOP>
A; Cross references: GB: XO2677; NID:g49897; PIDN:CAA26506.1; PID:g49898
A; Cross references: GB: XO2677; NID:g49897; PIDN:CAA26506.1; PID:g49898
A; Cell. Blochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Fitle: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
A; Accession: A26086
A; Molecule type: mRNA
A; Residues: 1-929 < KKO2
A; Residues: 1-929 < KKO2
A; Residues: 1-929 < KKO2
A; Cross references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
A; R: Applic, R: A; Addersson, M; Lodish, H.F.
J: Biol: Chem. 262, 8035-8040, 1987
Title: Structure and organization of the murine band
A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
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A;Residues: 11-466,'S',468-929 <DEM>
A;Cross.references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
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Pred. No. 1.3e-05;
0; Mismatches 1; Indels
                               A; Reference number: A25314; MUID:85268011; PMID:2410791
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Pred. No. 0.25;
3; Mismatches
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Best Local Similarity 95.0%;
Matches 19; Conservative (
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A; Residues: 1-844 <COX>
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A30816 band 3 anion transport protein (clone pBIIIC1) - chicken

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Gaps

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2003, 11:41:03 ; Search time 17.25 Seconds
(without alignments)
111.500 Million cell updates/sec Run on:

US-10-087-464-4 112 1 DRILLLFKPPKYHPDVPYVK 20 Title: Perfect score: coring table: edneuce:

283308 seqs, 96168682 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	band 3 anion trans	band 3 anion trans	band 3 protein - m	נ	ო	3	3-related	-related	band 3-related pro	Q.	anion exchanger 3,	band 3-related pro	erythrocyte anion	probable sodium bi	hypothetical prote	sodium bicarbonate	anion exchanger 3	acid phosphatase (		3 anion t			acid phosphatase (	Na+ bicarbonate co	probable histone d	hypothetical prote	methylaspartate am	sporulation specif	sodium bicarbonate
	ID	взни	A33810	A25314	150159	A30816	A25104	A34911	A31789	A56764	\$21086	A42497	B34911	A33638	T37460	T22491	T31336	I38496	B84540	S59861	S24318	QQBE40	H84669	A59200	PC7034	B75095	H71071	T43810	694	T13962
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æ	Query	100.0	4 96	, u	, (7)	73.2	66.1	66.1	66.1	66.1	66.1	60.7	60.7	60.7	58.9	58.9					4		ω,	43.8			2	42.9		42.9
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T14110 T14031	F69019 B84146	T04599	T30143	E72237	G82329	T23748	AH1642	C42327	A28451	A41734	A59201	S11967
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1035	234	466	137	306	468	1156	77	214	403	406	431	434
42.9	42.0	42.0	41.1	41.1	41.1	41.1	40.6	40.2	40.2	40.2	40.2	40.2
4 4 8 8	47	47	46	46	46	46	45.5	45	45	45	45	4.5
30	32	34	36	37	38	39	40	41	4.2	43	44	45

RESULT 1 B3HU band 3 anion transport protein, erythrocyte - human band 3 anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
C;Species: Homo sapiens (man) C:Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C;Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; R:IMX, S.E.: John, K.M.; Kopito, R.R.; Lodish, H.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989 A:Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange
A; Reference number: A36218; MUID:90083213; PMID:2594752
A. Status: preliminary A. Molecule type: mRNA
 A; Residues: 1-911 <lux> A; Cross-references: GB:M27819; NID:9178215; PIDN:AAA35514.1; PID:9178216</lux>
R:Tanner, M.J.A.; Martin, P.G.; High, S. Blochem. J. 256, 703-712, 1988
A; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tr
A. Accession: S0374
A; Molecule type: mRNA A: Residues: 1-55, 'E', 57-911 <tan></tan>
A;Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714
A; Title: Localization of the gene for the erythroid anion exchange protein, band 3
A;Reference unuber: 139408; MULD:88031311; PMID:34/0270
A; Molecule type: DNA
A; Residues: 37-56 <sho1> A: Cross-references: GB:M16978; NID:9178217; PIDN:AAA51670.1; PID:9178220</sho1>
A;Accession: 139409
A; Molecule type: DNA A; Residues: 118-161 <sho2></sho2>
A;Cross-references: GB:M16979; NID:q178218; PIDN:AAA51671.1; PID:g553169
A) Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Ide
A; Accession: A22237; MOID: 7021100; MILES
A; Molecule type: protein
R; Mawby, W.J.; Findlay, J.B.C.
Biochem. J. 205, 465-475, 1982 A: mitle: Characterization and partial sequence of d1-iodosulphophenyl isothiocyanate
A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Molecule type: protein
A; Residues: 43/74/3;30U-304, D.,300-309 NEWNY R; Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
J. Biol. Chem. 258, 7981-7990, 1983

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A, nuurycki, K.E.; Shull, G.E. J. Biol. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced for A;Reference number: A33810; MUD:89255254; PMID:2722777
C:Comment: Band 3 has at least two functional domains. Its integral domain mediates a ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                        A;Cross-references: GDB:119874; OMIM:109270
A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
C;Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transfr: F;1-403/Region: cytoskeletal protein binding
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C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A25314, A26086; I49524; B25104
R;KOpito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
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band 3 anion transport protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Accession: A33810
R;Kudrycki, K.E.; Shull, G.E.
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C;Superfamily: band 3 anion transport protein
C;Reywords: alternative splicing; transmembrane protein
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Pred. No. 5.5e-09;
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A; Residues: 1-848 <KUD>
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F;642/Binding site:
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F;701-721/Domain:
F;723-743/Domain:
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A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Molecule type: protein
A; Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN
A; Experimental source: erythrocyte
A; Experimental source: erythrocyte
A; Experimental source: erythrocyte
A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823, A; Note: a histidine residue essential for anion transport is suggested to be His-651, Hi
B; Okubo, K.; Kang, D.; Hamasaki, N.; Jenings, M.L.
J. Biol. Chem. 269, 1918-1926, 1994
A; Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4
A; Reference number: A49717; MUID:94124538; PMID:8294441
A; Accession: A49717
A; Molecule type: protein
A; Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 <OKU>
A; Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transport
B; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Blochem: 122, 577-585, 1997
A; Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
A; Accession: Potano.
A; Noces: Detail of the sites of band 3 protein in alkali-treated membranes: Fidel
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                                                                                                  A, Accession: A92430
A, Molecule type: protein
A; Racession: A92430
A; Molecule type: protein
B, Protein
B, Protein
A; Residues: 1-10, 'D', 12-68, 'E', 69-200 < KAU>
B; Brock, C.J.; Tanner, M.J.A.; Kempf, C.
B, A; Title: The human erythrocyte anion-transport protein
A; Reference number: A90323; MuID: 83308584; PMID: 6615451
A, Accession: A90323
A; Molecule type: protein
A; Residues: 559-630 < CRO>
A; Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport R; Kawano, Y; Okuboo, K; Tokunaga, F; Miyata, T; Iwanaga, S; Hamasaki, N.
B; Kawano, Y; Okubo, K; Tokunaga, F; Miyata, T; Iwanaga, S; Hamasaki, N.
A; Biol: Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
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A; Mealdues: 1-55, Ev. 57-69 < YAN2>
A; Realdues: 1-55, Ev. 57-69
A; Mote: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; Kang, D; Okubo, K.; Hemasaki, N.; Kuroda, N.; Shiraki, H.
A; Chem. 267, 19211-19217, 1992
A; A; A; A; A; More and A; More and
     Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte Reference number: A92430; MUID:83238395; PMID:6345535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: protein date of the state o
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t: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dimd 61-911

Molecule type: protein Accession: PC4403

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C.Accession: A30816
R.Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A.Title: Two different mRNAs are transcribed from a single genomic locus encoding the A; Preference number: A30816; MuID:89039870; PMID:3185555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A25104
R;Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Roy EMBO J. 5, 1205-1214, 1986
A;Title: Cloning and structural characterization of a human non-erythroid band 3-likk A;Reference number: A91039; MUID:86274622; PMID:3015590
A;Accession: A25004
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A;Molecule type: mRNA
A;Residues: 1-1234 «MUD-
A;Residues: 1-1234 «MUD-
A;Residues: 1-1234 «MUD-
A;Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
R;Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990
A;Tille: Functional expression and subcellular localization of an anion exchanger
A;Reference number: A35770; MUD:90319095; PMID:2371270
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990
J;Biol. Chem. 265, 462-471, 1990
A;Tille: CDNA cloning and tissue distribution of mRNAs for two proteins that A;Reference number: A34911; MUID:90094439; PMID:2294114
A;Reference number: A34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Species: Gallus gallus (chicken)
C.Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 82; DB 2; Ler
Pred. No. 0.00022;
); Mismatches 4;
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Pred. No. 0.0034;
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A) Residues: 1-865 < CDENY
A) Cross-references: GB:X03918; NID:g32120; PID
C) Superfamily: band 3 anion transport protein
C) Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
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65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 73.2%;
Best Local Similarity 78.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             band 3-related protein 2 - rat
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Best Local Similarity 65.0
Matches 13; Conservative
                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-922 <KIM>
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A tues preliminary; translated from GB/EMBL/DDBJ

A clues: 4-707, 'X',709-902 <RES.
EMBO J. 5, 1205-1214, 1986
A cluent b. B.: Showe, L.C.: Ballantine, M.: Palumbo, A.: Fraser, P.J.; Cloe, L.; Rovera EMBO J. 5, 1205-1214, 1986
A cluent b. B.: Showe, L.C.: Ballantine, M.: Palumbo, A.: Fraser, P.J.; Cloe, L.; Rovera EMBO J. 5, 1205-1214, 1986
A rice concerned and structural characterization of a human non-erythroid band 3-like procession: B25104
A; Residues: 11-466, 'S', 468-929 <CEM>A; Residues: 11-466, 'S', 468-929 <CEM>A; Cosa-references: GB:X03917; NID:G53042; PIDN:CAA27555.1; PID:G53043
C; Genetics:
A; Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/C; Reywords: transmembrane protein
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Mol. Cell. Biol. 8, 1327-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth.
A;Reference number: 150159; MUID:88216609; PMID:2835670
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                                                                   A, Residues: 1-929 < KKDPA
A, Residues: 1-929 < KKDPA
A, Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
A, Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
R, Koplito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A, Title: Structure of the murine anion exchange protein.
A, Recession: A26086, MUID:86034211; PMID:3840489
A, Accession: A26086, MUID:86034211; PMID:3840489
A, Accession: A26086, MUID:8034211; PMID:3840489
A, Residues: 1-929 < KKD2
A, Cross-references: GB:X29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
A, Foolito, R.R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 262, 8035-8040, 1887
A, Fittle: Structure and organization of the murine band 3 gene.
A, Fittle: Structure and organization of the murine band 3 gene.
A, Foolity A, Fittle: Structure and organization of the murine band 3 gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-844 <COX>
A;Residues: 1-844 <COX>
A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 108; DB 2; Length 92
Pred. No. 2.3e-08;
!: Mismatches 0; Indels
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band 3 anion transport protein (clone pBIIIC1) - chicken
   A; Reference number: A25314; WUID:85268011; PMID:2410791
A; Accession: A25314
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Pred. No. 0.0002;
0; Mismatches 4
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025 DRILLEKPPKYHPDVPFVK 844

d

1 DRILLLFKPPKYHPDVPYVK 20

Conservative

Local Similarity les 19; Conserv

Best Loc Matches

96.4%; 95.0%;

S RESULT

DRILLEKPPKYHPDVPYV 19

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Query Match 73.2%; Best Local Similarity 78.9%; Matches 15; Conservative

A; Accession: I50159

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53
16
                                                                                                                                                                                       'cgn2_C/ptodata/1/pubpa/USOC_PUBCOMB.pep:

'cgn2_C/ptodata/1/pubpa/USOC_PUBCOMB.pep:*

'cgn2_C/ptodata/1/pubpaa/USOC_NEW_PUB.pep:*

'cgn2_C/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

'cgn2_C/ptodata/1/pubpaa/USOB_NEW_PUB.pep:*

'cgn2_C/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*

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/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513375 seqs, 137303645 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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1 GMPWLSATTVRSVTHANALT 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 1, Appli Sequence 39328, A Sequence 3, Appli Sequence 6, Appli Sequence 8, Appli Sequence 8, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Description US-09-864-761-39328 US-10-066-320-2 US-10-087-464-6 US-10-087-464-8 US-09-920-804-2 US-09-920-804-4 US-09-734-674-2 US-10-274-990-2 US-09-728-137-4 US-09-728-137-8 US-09-728-137-2 US-09-734-674-4 US-10-274-990-4 % Query Match Length DB 1088 1088 1129 1129 100.0 Score Result

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Gaps

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Length 20; Indels

Score 104; DB 15; Pred. No. 2.2e-09; ; Mismatches 0;

ch 100.0%; Score 104; D Similarity 100.0%; Pred. No. 2.2 20; Conservative 0; Mismatches

Query Match Best Local Similarity

Matches

g δ

RESULT 2
US-10-087-464-22
'Sequence 22, Application US/10087464
'Publication No. US20030059436A1
'GENERAL INFORMATION:

16 53 51.0 570 12 US-10-017- 18 44.5 42.8 217 9 US-20-205- 19 44.5 42.8 217 9 US-10-001- 20 44 42.3 633 14 US-10-001- 21 44 42.3 875 14 US-10-001- 22 44 42.3 875 14 US-10-001- 23 44 42.3 891 14 US-10-001- 24 43 41.3 88 10 US-09-880- 25 43 41.3 138 10 US-09-880- 26 43 41.3 138 10 US-09-880- 27 43 41.3 138 15 US-10-237- 29 43 41.3 138 15 US-10-237- 30 43 41.3 138 15 US-10-237- 31 43 41.3 138 15 US-10-237- 32 43 41.3 138 15 US-10-106- 33 41.3 138 15 US-10-106- 34 41.3 138 15 US-10-106- 35 43 41.3 138 15 US-10-106- 36 43 41.3 138 15 US-10-106- 37 43 41.3 138 15 US-10-106- 38 43 41.3 138 15 US-10-106- 39 43 41.3 138 15 US-10-106- 30 43 41.3 138 15 US-10-106- 31 43 41.3 138 15 US-10-106- 32 43 41.3 138 15 US-10-106- 33 43 41.3 138 15 US-10-106- 34 41.3 13 13 10 US-09-880- 36 43 41.3 13 12 US-10-108- 37 43 41.3 13 10 US-09-880- 38 43 41.3 13 10 US-09-880- 39 43 41.3 13 10 US-09-880- 30 43 41.3 3170 15 US-10-128- 45 40.4 589 14 US-10-13- 41 43 41.3 3170 15 US-10-128- 45 40.4 589 14 US-10-128- 45 40.4 589 14 US-10-13- 40 40.4 589 14 US-10-13- 40 40.4	US-10-017-161-2064 Sequence 2064, Ap US-10-205-823-373 Sequence 177, App US-09-811-217 Sequence 177, App US-10-001-852-5 Sequence 2, Appli US-10-001-852-6 Sequence 6, Appli US-10-001-852-6 Sequence 6, Appli US-09-880-503-1 Sequence 7, Appli US-09-880-503-1 Sequence 7, Appli US-09-880-503-1 Sequence 12, Appli US-09-980-503-9 Sequence 12, Appli US-10-237-867-12 Sequence 12, Appli US-10-237-861-12 Sequence 12, Appli US-10-237-864-12 Sequence 6, Appli US-10-137-865-4 Sequence 161, Appli US-10-10-80-865-4 Sequence 161, Appli US-10-10-10-80-865-4 Sequence 10360, Appli US-10-13-11-11-11-11-11-11-11-11-11-11-11-11-	ALIGNMENTS  ULT 1  10-087-464-1  tequence 1, Application US/10087464  ubblication No. US20030059436A1  tepuence 1, Application US/10087464  ubblication No. US20030059436A1  tepuence 1, Application S. US20030059436A1  APPLICAT: Ob, Steven  APPLICANT: Liu, David  APPLICANT: Liu, Nercong  APPLICANT: Liu, Nercong  TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There  CURRENT APPLICATION NUMBER: US/10/087,464  PRIOR APPLICATION NUMBER: US 06/272,930  PRIOR APPLICATION NUMBER: US 06/272,930  PRIOR APPLICATION NUMBER: US 06/272,930  PRIOR FILING DATE: 2001-03-02  SOFTWARE: PATE THE THE THE THE THE THE THE THE THE T
44.5 44.7 45.2 8 44.4 44.3 44.4 44.3 44.4 44.3 44.4 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3 44.3	-	nn US/100 100594367 tthar en ad ad ad ad an an an an an an an an an an an an an
- 프라프라드 단대대 프라트라프라트웨어가 제한 학생 학생 전쟁이 가지 그는 그 그 그는 그를 모고 모고 모고 모임을 모임 모든 모임을 모임	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 1 1087-464-1 10ence 1, Applicatic 11 Applicatic ERAL INFORMATION, A PLICANT: Chisht, A PLICANT: Chisht, A PLICANT: Chisht, A PLICANT: Chisht, A PLICANT: Liu, Davi PLICANT: Liu, Davi PLICANT: Liu, Davi PLICANT: Liu, Carv PLO ON INVENTION NOW IOR FILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 MBER OF SEQ ID NOS: FTAARE: PATEILING DATE: 20 PLOSTH: 20 PLOSTH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-21
INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Singel, David J.
APPLICANT: Singel, David J.
TITLE OF INVENTION: Method for Determining Physiological
FILE REFERENCE: 1818.1030-003
CURRENT PELLOR ON UNMER: US/10/066,320
CURRENT FILING DATE: 2002-01-31
PRIOR PELLORION NUMBER: DCT/US00/21101
PRIOR PELLORION NUMBER: US60/146,680
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SCPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 911
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IN BRAIN, SIGNAL = 1.5
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 39328
LENGTH: 86
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red. No. 1.1e-07;
Mismatches 0;
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Pred. No. 9.6e-09;
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Publication No. US2003002267A1
GENERAL INFORMATION:
APPLICANT: Stamler, Jonathan S.
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APPLICANT: Chishil, Athar
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100.0%;
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illarity 100.0%;
Conservative 0
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Best Local Similarity
Matches 20; Conserv
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OTHER INFORMATION:
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                                                                                                             APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S123/7/019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: US 60/180,312
PRIOR FILING DATE: US 60/207,456
PRIOR FILING DATE: US 60/207,456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; DB 15;
4.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR RELING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR PILING DATE: 2000-09-27 PRIOR PELING DATE: 2000-09-27 PRIOR PILING DATE: 2001-01-30 PRIOR PELING DATE: 2001-01-30 PRIOR PELICATION NUMBER: PCT/USO1/00667 PRIOR PELING DATE: 2001-01-30 PRIOR PELING PEL
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100.0%; Score 104;
Best Local Similarity 100.0%; Pred. No. 4
Matches 20; Conservative 0; Mismatche
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PRIOR APPLICATION NUMBER: US 06/272,930
PUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 22
LENTH: 42
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Patent No. US20020048763A1
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
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   Chishti, Athar
                                                                                          Goel, Vikas
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-087-464-22
                                                           Liu, David
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APPLICANT:
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Pred. No. 0.081;
3; Mismatches 5; Indels
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                 CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/115,954
PRIOR PILING DATE: 1998-07-15
PRIOR PELING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1997-07-16
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400272.5
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 1998-02-09
PRIOR PLICATION NUMBER: EP 98400454.9
PRIOR FILING DATE: 1998-02-26
NUMBER OF SEO ID NOS: 10
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509 GLPWFVAATVLSITHVNSL 527
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Matches 11; Conservative
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US-09-728-137-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 4
LENGTH: 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-728-137-8
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                                                                                TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
ENGINE PATENCE PATENCE
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APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
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100.0%; Pred. No. 1.1e-07;
iive 0; Mismatches 0;
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Pred. No. 1.1e-07;
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APPLICANT: Steven Charles Jupe
APPLICANT: Christopher John Rawlings
APPLICANT: Trudy Rachel Doe
TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antoine Michel Alain Bril
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Patent No. US200100029031A1
GENERAL INFORMATION:
APPLICANT: Walter F. Boron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 100.0% Matches 20; Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
Liu, David
Goel, Vikas
                                                    Li, Xuerong
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US-09-728-137-4
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APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 4, Application US/10274990

Sequence 4, Application US/2034991

Bublication No. US20030054491A1

GENERAL INFORMATION:

APPLICANT: WELL MING-HUI et al

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROFIENS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES.ENCODING HUMAN TRANSPORTER PROFIENS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES.ENCODING HUMAN TRANSPORTER PROFIENS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES.ENCODING HUMAN TRANSPORTER PROFIENS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES.ENCODING HUMAN TRANSPORTER PROFIENS,

FILE REFERENCE: CL001018 DIV

CURRENT FILING DATE: 2002-10-22

PRIOR FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 1085
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Patent No. US20020064846A1
GENERAL INFORMATION:
APPLICAMT: Seino, Susumu, JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
FILE REFERENCE: GP4
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 1088
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TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%; Score 66; DB 15; Length 1085;
nilarity 57.9%; Pred. No. 0.085;
Conservative 3; Mismatches 5; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
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US-09-920-804-2

Sequence 2, Application US/09920804

Patent No. US20020064846A1

SEMERAL INFORMATION:
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840 GLPWFVAATVLSITHVNSL 858
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837 GLPWFVAATVLSITHVNSL 855
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Best Local Similarity 57.99
Matches 11; Conservative
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; ORGANISM: Mus musculus
US-09-920-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORGANISM: Mus musculus US-10-274-990-4
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Best Local Similarity
Matches 11; Conserv
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US-09-920-804-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI, Ming-Hui et al
APPLICANT: WEI MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOLO18
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOCTWARE: FASUSEQ for Windows Version 4.0
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                                                                                                                                                                                                                    APPLICANT: Xavier Martin
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Trudy Rachel Doe
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REPERENCE: 6H 30409-D1
CURRENT APPLICATION NUMBER: US/97728,137
CURRENT PELING DATE: 2000-12-01
PRIOR PAPLICATION NUMBER: 09/115,954
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: EP 97401714.7
PRIOR APPLICATION NUMBER: EP 97401713.9
PRIOR FILING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EP 98400272.5
PRIOR APPLICATION NUMBER: EP 98400454.9
PRIOR PILING DATE: 1998-02-09
PRIOR SEULING DATE: 1998-02-09
PRIOR SEULING DATE: 1998-02-09
PRIOR SEULING DATE: 1998-02-09
PRIOR SEULING DATE: 1998-02-06
NUMBER OF SEO ID NOS: 10
                                             Sequence 2, Application US/09728137
Patent No. US20010029031A1
GENERAL INFORMATION.
APPLICANT: Walter F. Boron
APPLICANT: Antoine Michel Alain Bril
APPLICANT: Nassirah Khandoudi
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839 GLPWFVAATVLSITHVNSL 857
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; ORGANISM: Mus musculus
US-09-734-674-4
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US-09-728-137-2
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LENGTH: 1085
                  US-09-728-137-2
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Length 1088

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US-09-734-674-2

Sequence 2, Application US/09734674

Fatent No. US20020081648A1

Fatent No. US20020081648A1

FATELE OF INVENTION: ISCLATED BUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REPERENCE. CLOOLO18

CURRENT APPLICATION UNUMBER: US/09/734,674

CURRENT PILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 1129

TYPE: PRT

CREATER: Human

CSCOURTER: Human
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Publication No. US20030054491A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USCLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018 DIV
CURRENT APPLICATION NUMBER: 2010-10-22
PRIOR APPLICATION NUMBER: 09/734,674
PRIOR APPLICATION NUMBER: 09/734,674
NUMBER OF SED ID NOS: 4
SOFTWARE: FRSESEQ FOR WINDOWS VERSION 4.0
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Pred. No. 0.089;
Score 66; DB 9; Length 1088;
Pred. No. 0.086;
                                                        5; Indels
                                                     3; Mismatches
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881 GLPWFVAATVLSITHVNSL 899
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881 GLPWFVAATVLSITHVNSL 899
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Best Local Similarity 57.9%; Pr
Matches 11; Conservative 3;
  ch 63.5%;
1 Similarity 57.9%;
11; Conservative
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Matches 11; Conserv
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; ORGANISM: Human
US-10-274-990-2
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Search completed: September 3, 2003, 11:53:43 Job time: 17.5 secs

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Sequence 96, Appl
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Sequence 11, Appl
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                                                                                                                  September 3, 2003, 11:42:58; Search time 15.75 Seconds (without alignments) 53.728 Million cell updates/sec
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Sequence 2, Al
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Sequence 48,
Sequence 1, P
Sequence 3, P
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Sequence 80,
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
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Match Length DB
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No.
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Patent No. 5188829 Sequence 47, Appl Sequence 27453, A Sequence 27117, A Sequence 4, Appli Sequence 4, Appli Sequence 22525, A Sequence 17821, A Sequence 12, Appl Sequence 17, Appl Sequence 17, Appl Sequence 740, Appl Sequence 740, Appl Sequence 740, Appl Sequence 28044, A			gth 714; Indels 0; Gaps 0;		·
5188829-1 US-08-560-098A-47 US-09-252-991A-27453 US-09-252-991A-24117 US-07-943-843-4 US-08-347-003-4 US-08-252-991A-25255 US-09-252-991A-25255 US-09-252-991A-17821 US-08-459-346-12 US-08-402-542-12 US-08-402-542-12 US-08-402-542-12 US-08-107-532A-3890 US-09-205-258-740 US-09-205-258-740 US-09-205-258-740	ALIGNMENTS	09115954B  irah stopher J COMPOUNDS : US/09/115,954B :07-15 :: EP97401714.7 :07-16	Score 66; DB 3; Len Pred. No. 0.032; 3; Mismatches 5;	.t. 19 	15954B h her J POUNDS iS/09/115,954B
411.3 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 401.4 40		pplication US/0 MATION: oron, Walter F ril, Antoine M handoudi, Nassi artin, Xavier upe, Steven C awlings, Christu ce, Trudy R ENTION: NOVEL C CE: GH: 30409 ICATION NUMBER: NG DATE: 1998-0 ICATION NUMBER: NG DATE: 1997-0 O ID NOS: 10 tentin Ver: 2.0	h Similarity 57.9%; 11; Conservative	GMPWLSATTVRSVTHANAL  :         :    :  GLPWFVAATVLSITHVNSL	954-8 8. Application US/09115954B 5. 6200776 INPORMATION' WIT: Borio, Walter F NT: Bril, Antoine M NT: Khandoudi, Nassirah NT: Martin, Xavier NT: Jupe, Steven C NT: Doe, Trudy R FINVENTION: NOVEL COMPOUNDS FERENCE: GH-30409 APPLICATION NUMBER: US/09/115,954B
28 33 33 33 33 33 33 33 33 34 40 40 40 40 40 40 40 40 40 40 40 40 40		RESULT 1 US-09-115-954-4 Sequence 4, A Sepulcant: APPLICANT: APPLIC	Query Matc Best Local Matches	Δy 1 Db 509	RESULT 2 US-09-115-954-8 US-09-115-954-8 Sequence 8, Applica' Patent No. 6200776 GENERAL INFORMATION APPLICANT: Bril, A APPLICANT: Martin, APPLICANT: DOG, Tri
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881 GLPWFVAATVLSITHVNSL 899
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838 LPWYVAATVISIAHIDSL 855
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Bost Local Similarity 5/...
Action 11; Conservative
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US-09-136-652-2
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US-09-734-674-2
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       US-09-734-674-4
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Patent No. 6498022

GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018
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APPLICANT: BAIL, Antoine M
APPLICANT: BAIL, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Martin, Xavier
APPLICANT: Wawlings, Christopher J
APPLICANT: BANINGS, Christopher J
APPLICANT: BOO, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTH: 1044
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UNDRENT FILING DATE: 2000-12-13
NUMBER OF EGG ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09115954B Patent No. 6200776 GENERAL INFORMATION:
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827 GLPWFVAATVLSITHVNSL 845
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839 GLPWFVAATVLSITHVNSL 857
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Best Local Similarity 57.9%;
Matches 11; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-09-115-954-8
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LENGTH: 1085
                                                                                                                     LENGTH: 1032
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Sequence 2, Application US/09734674

Sequence 2, Application US/09734674

Fatent No. 6498022

GENERAL INFORMATION:

APPLICANT: WEL, Ming-Hui et al

ATTLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REPERENCE: CLOOL018

CURRENT APPLICATION NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastesEQ for Windows Version 4.0

SEQ ID NO 2
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Length 1085;
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Query Match 63.5%; Score 66; DB 4; Best Local Similarity 57.9%; Pred. No. 0.052; Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 66; DB 4;
Pred. No. 0.054;
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Pred. No. 45;
4; Mismatches
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Patent No. 6096517

GENERAL INFORMATION:
APPLICANT: BRILL, ANTOINE
APPLICANT: HAMDOUL). NASSIRAH
APPLICANT: MARTIN, XAVIER
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30010
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT APPLICATION NUMBER: BP 974019473.3
EARLIER PETLING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FALLING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PRESENCE: BP SESSEQ FOR WINDOWS VERSION 3.0
SEQ ID NO 2
LENGTH: 1079
TYPE: PRT
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Gaps
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                                                                                                                                                                                                                                                   Length 138;
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; GENERAL INFORMATION:

APPLICANT: NISSIN FOOD PRODUCTS CO., Ltd.

; TILLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR

; FILE REFRENCE: 050979

; CURRENT APPLICATION NUMBER: US/09/101,272G

; CURRENT FILING DATE: 1998-07-08

; PRIOR APPLICATION NUMBER: JP 1059/1996

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PALENTIN PARENTING DATE: 1996-01-08

; NUMBER OF SEQ ID NOS: 107

; SEQ ID NO 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORDATION:
GENERAL INCORDATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: Q50979
CURRENT APPLICATION NUMBER: U5/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin version 3.1
SEQ ID NO 80
LENGTH: 194
                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                 41.3%; Score 43; DB 43.8%; Pred. No. 18; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: ATFHI chimeric protein US-09-101-272G-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: misc_feature
; OTHER INFORMATION: ATF domain of uPA
US-09-101-2726-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/09101272G Patent No. 6509445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-101-272G-73 ·
Sequence 73, Application US/09101272G
Patent No. 6509445
  TELECOMMUNICATION INFORMATION:
                                     TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                 :|| ||| :: ||:
75 LPWNSATVLQQTYHAH 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|| ||| :: ||:
73 LPWNSATVLQQTYHAH 88
                                                                                                                                                                                                                                                                                                                                       2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 MPWLSATTVRSVTHAN 17
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
WOLECULE TYPE: protein
US-08-797-689-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43.8 Matches 7; Conservative
                                                                                                                                                                                                                                              Query Match 41.3
Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-101-272G-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    ) NAME/KEY: misc_feature
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                               APPLICANT: NISSIN FOOD Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR PLICATION NUMBER: JP 1059/1996
PRIOR FLILOM DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PATENTIN POSI: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-QAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.3%; Score 43;
Best Local Similarity 43.8%; Pred. No.
Matches 7; Conservative 4; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhone-Poulenc Rorer Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/FR93/00085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/256,927 FILING DATE: 28-JUL-1994 APPLICATION NUMBER: FR 92/01064 FILING DATE: 31-JM-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/FR93/0008
                  Sequence 62, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08797689 Patent No. 5876969 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 500 Arcola Road, 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :|| ||| :: ||:
30 LPWNSATVLQQTYHAH 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collegeville
                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
US-09-101-272G-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-797-689-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                           SEQ ID NO 62
                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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New York
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US-08-597-236-11
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                Score 43; DB 4; Length 200; Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.3%; Score 43; DB 4; Length 208; ilarity 43.8%; Pred. No. 29; Conservative 4; Mismatches 5; Indels
                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICAMT MISSIN FOOD Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REPERENCE: 050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: UP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Version 3.1
SEQ ID NO 98
LENGTH: 208
                                                                                                                                                                                                                                                                                        APPLICATE: MISSIN FOOD PRODUCTS CO., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: 6050979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: ATFHI-CL chimeric protein US-09-101-272G-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: ATFHI-ML chimeric protein US-09-101-2726-98
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 98, Application US/09101272G; Patent No. 6509445; GENERAL INFORMATION:
                                                                                                                                                                                                                  US-09-101-272G-96
; Sequence 96, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
                                                                                                                     :|| ||| :: ||:
92 LPWNSATVLQQTYHAH 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|| ||| : ||:
73 LPWNSATVLQQTYHAH 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                              2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 96
LENCTH: 201
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 MPWLSATTVRSVTHAN 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :|| ||| :: ||:
73 LPWNSATVLQQTYHAH 88
                Query Match 41.3%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 41.3
Best Local Similarity 43.8
Matches 7; Conservative
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Best Local Similarity
7; Conserve
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US-09-101-272G-98
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RESULT 13

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Sequence 11, Application US/08597236
Fatent No. 5733765
GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTERIA PRODUCING
TITLE OF INVENTION: EXPOLYSACCHARIDES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
CORRESPECT: 1155 Avenue of the Americans
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/597,236 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CAPLICATION NUMBER: US/08/746,682A
FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LACTIC BACTERIA PRODUCING EXOPOLYSACCHARIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 54;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americans
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: EP 95201669.9 FILING DATE: 20-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08746682A Patent No. 5786184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTER
TITLE OF INVENTION: EXOPOLYSACCHA
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 MPWFILTVLATLEHATAI 177
                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 MPWLSATTVRSVTHANAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Fanucci A., Allan REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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APPLICANT: SCHRIEDER, JOHANNES
APPLICANT: SCHRIEDER, JOHANNES
APPLICANT: HEINZEL-WIELAND, REGINA
APPLICANT: SAUNDERS, DEREK J.
TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
TITLE OF INVENTION: INHIBITING EFFECT
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB 1; Length 360;
Pred. No. 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSENCE Evenson, McKeown, Edwards & Lenahan STREET: 1200 G Street, N. W. Suite 700 CTIY: Washington, D.C. COUNTRY: U.S. COUNTRY: U.S. COUNTRY: U.S. COUNTRY: U.S. COMPUTER READABLE FORM: MEDIOW TYPE: Floppy disk COMPUTER: IDM PC COMPATIBLE OF STREET: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/093,741 FILING DATE: 12-JUL-1993 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: DE P43 23 754.1 FILING DATE: 15-JUL-1993 ATTORNEY/AGENT INFORMATION: NAME: EVANS, JOSEPH D. REGISTRALION NUMBER: 26,269 REFERENCE/DOCKET NUMBER: 148/41345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: AMOLECULE TYPE: Protein

MOLECULE TYPE: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 MPWFILTVLATLFHATAI 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 38.9%;
Matches 7; Conservative
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INFORMATION FOR EEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acids
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US-08-093-741-83
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US-08-093-741-83
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41.3%; Score 43; DB 1; Length 365;

Query Match

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Best Local Similarity 43.8%; Pred. No. 54;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps

Qy 2 MPWLSATTVRSVTHAN 17

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Db 26 LPWNSATVLQGTYHAH 41

Search completed: September 3, 2003, 11:52:26

Job time: 16.75 secs
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Human erythrocyte
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Human erythrocyte
Human Band 3 prote
Human Band 3 prote
Human Band 3 prote
Novel human secret
Aouse kidney cell
A. tigrinum AB2 pr
A. tigrinum AB2 pr
A. tigrinum AB2 pr
Drosophila melanog

hNBC3 protein sequ Human brain-derive Murine Na+-driven Human Na+-driven Human transporter Human transporter

human diagno

Novel

hNBC3a protein seq

hNBC3 protein sequ

Human secreted pro Human secreted pro Human secreted pro Human heart muscle Human NT2-2A prote Drosophila Na+ dri Drosophila Na+ dri Drosophila Na+ dri Drosophila Na+ dri

Larval viability a Human protein sequ Human polypeptide Human transporter

Drosophila melanog

melanog Na+ dri Na+ dri

Drosophila Drosophila Drosophila

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
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AAB46914
AAE29343
                                                                       AAE29344
AAU30825
AAP60645
AAW90262
AAW90261
ABB63733
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AAW74409
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AAB20659
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 Human Band 3 pepti
Human liver peptid
Peptide #6645 enco
Protein #6029 enco
Human brain expres
Human bone marrow
Peptide #6670 enco
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAE29349
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1 GMPWLSATTVRSVTHANALT 20
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Maximum DB seq length: 200000000
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Score 104; DB 23; Pred. No. 5.1e-10; Mismatches

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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
sequence is human Band 3 protein ectoplasmic domain
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21-SEP-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GS-0236359.
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                                                                                                                                         Query Match
Best Local Similarity
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30-JUN-2000;
03-AUG-2000;
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                                                                                    The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPO-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and harmful side effects and drug resistance that may be due to non specific therapeutic approaches. The invention is useful in gene tharapy. The present invention also provides a vaccine for malaria. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;
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100.0%; Pred. No. 2.1e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE29349 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 58; 163pp; English
                               Claim 1; Page 84; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002; 2002WO-US06415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protozoacide; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oh ss,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-759814/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200270542-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAE29349
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                                                                                                                                                                                                                                                                      The invention relates to a single exon nucleic acid probe (SENP) (I) for massuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human liver single exon encoded peptides of the invention.
Note: The sequence information for this patent does not appear in the
printed specification but was obtained in electronic format directly
                                                                               Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 104; DB 22; ilarity 100.0%; Pred. No. 1.2e-09; Conservative 0; Mismatches 0;
                                                                                                                                                                                               Claim 27; SEQ ID No 32714; 658pp; English.
WPI; 2001-488898/53.
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es 20; Conserv
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Matches
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Rank DR;

Chen W,

Hanzel DK,

2000US-0180312

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
               Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzhelmer's disease; multiple sclerosis; schizophrenia;
epllepsy; cancer.
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                                                   Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; SEQ ID No 25800; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W, Rank DR;
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2000US-0608408.
2000US-0632366.
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2000GB-0024263
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Matches 20; Conservative
                                                                                         congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 AA;
                                                                                                                                                                  WO200157274-A2.
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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0
                                                                                                                                                                                                                                                             Peptide #6645 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 86;
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100.0%; Pred. No. 1.2e-09;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W, Rank DR;
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                                                                                                                                                ABB39139 standard; Peptide; 86 AA
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                 GMPWLSATTVRSVTHANALT 20
                                     04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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               7
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ABB24030
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Hanzel DK,
                          Hanzel DK,
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nes 20; Conserv
                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                   genetic disorder
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                      Seguence
                                                                                                                                                                                      Query Match
                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                           Probe;
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Matches
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                                                                                                                                                                                                                                                                    RESULT 8
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                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 32683
                                                                                                                                                                                                                Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                       Length 86;
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                                                                                                                                                                                                                                                                                                                       100.0%; Score 104; DB 22; 100.0%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microarray; cancer; leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                    Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                      AAM72377 standard; Protein; 86 AA
                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
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                                                                   26-MAY-2000; 2000US-0207456.
30-UUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0608408
                                           2001WO-US00667
                                                            2000US-0180312
                                                                                                                                                                                                                                                                                      the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                               Local Similarity 100.
                                                                                                                                                   Penn SG, Hanzel DK,
                                                                                                                                                                   WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                       86 AA;
        WO200157275-A2
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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30-JUN-2000;
                                           30-JAN-2001;
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                          09-AUG-2001
                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                           34
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                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                              brains
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #6670 encoded by probe for measuring placental gene expression.
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                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 104; DB 22;
100.0%; Pred. No. 1.2e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                             analyzing gene expression in human bone marrow
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                                                             Chen W, Rank DR;
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(MOLE-) MOLECULAR DYNAMICS INC
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2000US-0608408.
2000US-0632366.
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2000US-0236359.
2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes, Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of
predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                      Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spatially addressable set of single exon nucleic acid probes, used to
                                                                                            Gaps
                                                                                                                                                                                                                                                                                         Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
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                                                                    100.0%; Score 104; DB 22; 100.0%; Pred. No. 1.2e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measure gene expression in human lung samples
                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank DR;
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2000US-234687P.
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2000US-0608408.
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                                                                                Local Similarity
                                              86 AA;
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the array; identifying exons in a eukaryotic genome, comprising

(a) algorithmically predicting at least one exon from genomic sequences
of the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
in the above mentioned microarray; assigning exons to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene
expression analysis, and for identifying exons in a gene, particularly
using human lung derived mRNA and for the study of lung disease
(COPD), interstitial lung disease (ILD), familial idiopathic pulmonary
tibrosis, neurofibromatosis, tuberous sclerosis, gaucher's disease,
Niemann-Pick disease, Hermansky-budlak syndrome, sarcoidosis, pulmonary
hypertension
and hyaline membrane disease. The present sequence is a peptide/protein
where men a single exon probe of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
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100.0%; Pred. No. 1.2e-09;
ive 0; Mismatches 0;
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(first entry)
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N-PSDB; AAQ15172.
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                                                                                                                                      The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COCH) code for a peptide which is immuno-reactive with antibodies to senescent cell acting an action of the binding of senescent cell in the antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell igG to senescent cells in vitro or in vivo. The prods. Can be used in to examine various physiological, blochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as haemolytic anaemia, sickle cell anaemia, and idiopathic through the senescent cell anaemia, and idiopathic as rheumatoid arthritis and systemic lupus erythematosus; and other diseases such as those involved in malaria and cancer. More specifically, the prods. As a series of the competic and pharmacoutical and concern the content of the concern the content of the content of the concern that the consertic and pharmacoutical content of the content 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   separating anions from a gas or liquid, or diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      compsns., diagnostic kits, and methods for detecting or measuring Abs to SCA, studying cellular ageing and autoimmune mechanisms,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating
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Is BA, Grichtchenko II, Romero MF, Schmitt BM;
    mechanisms, separate anions and treat auto-immune disease
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                                                                             Disclosure; Fig 1; 74pp; English.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        certain diseases
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Choi I, Davis BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-059743/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYYA ) UNIV YALE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-1999
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Sussman CR;
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                                                                                                                                This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucome and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate NBC mediated partners that blod NBC, (iii) in methods to identify and isolate binding partners that blod NBC, (iii) in methods to identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; PER; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock mycocardial depression; panorcatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for determining the predominant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erythrocyte band 3 anion transporter protein; human; hypercoagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 104; DB 20;
100.0%; Pred. No. 2.1e-08;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720 GMPWLSATTVRSVTHANALT 739
                                                                     Example 1; Fig 5; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-2000; 2000WO-US21101.
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(RERE-) RES & DEV INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
disorders mediated by NBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-183002/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stamler JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-MAY-2001
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       involves obtaining electron paramagnetic resonance (CER) or UV spectra of iron-nitrosyl hemoglobin derivatives formed by incubation of limiting nitro oxide (NO) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the hemoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antininflammatory; antiathmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoagulable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, septicemia as a complication of uninary tract infection and patients with ischemia, patients in a sickle cell crisis and for treating inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide; malarial infection; drug resistance; vaccine; gene therapy.
                                                                                                                                                                                                                       conditions such as arthritis, asthma, cerebritis, bronchitis and vasculitis. The methods are also used for preserving red blood cells
                                                                                                                                                                                                                                                                                                                                                Gaps
physiological effect of a composition comprising hemoglobin which
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                                                                                                                                                                                                                                                                                                                 Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE29343 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                            720 GMPWLSATTVRSVTHANALT 739
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                                                                                                                                                                                                                                                   which can be used in therapy
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                                                                                                                                                                                                                                                                                                                             Local Similarity 100. tes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Band 3 protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chishti AH, Oh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI > 2002-759814/82.
                                                                                                                                                                                                                                                                                  911 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Band 3 protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                     Sequence
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Matches
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inhibiting the particular interactions between the malarial parasite and

The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon

New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection

N-PSDB; AAD46978.

Disclosure; Page 102-105; 163pp; English,

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a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   malarial infection; drug resistance; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
                                                                                                                                                                  Gaps
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                                                                                                                                   911;
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                                                                                                                                                                  Indels
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Pred. No. 2.1e-08;
; Mismatches 0;
                                                                                                                                  Score 104; DB 23;
Pred. No. 2.1e-08;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
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                                                                                                                                                                                                                                                                                                                  AAE29344 standard; Protein; 911 AA.
                                                                                                                                                                                                                  720 GMPWLSATTVRSVTHANALT 739
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                                                                                                                                100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002WO-US06415.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Band 3 polypeptide;
protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Human Band 3 protein #2.
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                                                                                                   911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAD46979
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                                                                                                     Seguence
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                                                                                                                                                                                                                                                                                     RESULT 14
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying at therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                             Human, vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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100.0%; Pred. No. 2.3e-08;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                             Novel human secreted protein #1316.
                                                                                                     AAU30825 standard; Protein; 962 AA
720 GMPWLSATTVRSVTHANALT 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                                                      16-APR-2001; 2001WO-US08656.
                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.'
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611725/70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                   WO200179449-A2.
                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                        18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2001,
                                                                                                                                      AAU30825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                      RESULT 15
                                                                                         AAU30825
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Gaps

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Indels

Search completed: September 3, 2003, 11:46:11 Job time: 50.5 secs

771 GMPWLSATTVRSVTHANALT 790

1 GMPWLSATTVRSVTHANALT 20

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OBGZW1 OFFICE STATE OFFICE OFFI
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                            099416 homo sapien
013717 homo sapien
0955w2 drosophila
08mrk3 drosophila
08iqd4 drosophila
08iqd6 drosophila
08iqd5 drosophila
08iqd5 drosophila
  brachydanio
                               homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Programmer of TISSUE—Colon;

AT Ye.H., Binder H.J., Rajendran V.M.;

AT Protein (AEI) mRNA from rat colon.",

Buble (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AY030082; AAK38733.1; -.

BR InterPro; IPR001717; Anion_exchange.

InterPro; IPR001717; Anion_exchange.

BR InterPro; IPR001717; Anion_exchange.

BR InterPro; IPR001717; Anion_exchange.

BR TIGREPAS; TIGR0034; ae; 1.

BR TIGREPAS; TIGR0034; ae; 1.

BR PROSTEE; PS00219; ANION_EXCHANGER_1; 1.

BROSTEE; PS00219; ANION_EXCHANGER_2; 1.

CROUGENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                      Q9erp5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.9%; Score 91; DB 11; Length 849; 95.0%; Pred. No. 3.7e-06; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
Band 3 anion exchange protein.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                       849 AA.
                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
QBJFT9
Q9ERP4
Q9ERP4
Q9ERP6
Q99416
Q99416
Q91317
Q91317
Q910D4
Q810D5
Q810D5
Q9148
Q962W1
Q962W1
Q962W1
Q962W1
Q962W1
Q962W1
Q962W1
Q962W1
Q962W1
Q96WW1
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                                                                                                                                                                                                                                                                   Q9KKA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 95.0
nes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                        SEQUENCE FROM N.A.
61
61
61
57
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7.5
                                                                                                                                           Query Match
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Q91ZE7;
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Matches
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 RESULT
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Q99654 homo sapien
Q9uey6 homo sapien
P79877 lampetra ja
Q90579 gallus gall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9tu75 sus scrofa
Q8tag3 homo sapien
Q90710 gallus gall
Q9uey4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q91ze7 rattus norv
Q9tuq0 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       035225 cynomys lud
Q991t5 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9udjl homo sapien
Q91452 oncorhynchu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9xsw5 bos taurus
                                                                    3, 2003, 11:40:18; Search time 44.5 Seconds
(without alignments)
115.979 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
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Q9uey5 h
Q99654 h
                                                                                                                                                                                                       830525
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                     Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                   830525 seqs, 258052604 residues
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                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
                                                                                                           US-10-087-464-2
98
1 SVTHANALIVMGKASTPGAA 20
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Q90710
Q9UEY4
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Q9TUQ0
Q9XSW5
Q35225
Q99LT5
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Q99654
Q9UEY6
P79877
Q90579
Q9UDJ1
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                             SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                             sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
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sp_bacteriap:*
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Maximum DB seq length: 2000000000
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sp_rodent:*
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Match Length DB
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622
1129
1219
1227
1227
1241
1241
160
844
124
160
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733
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733
733
657
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653
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                                                                     Run on:
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DDA RET READ BR B DDA B

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TIGRFAMs; TIGRO0834; ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Hypothetical protein.
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                     80.6%;
84.2%;
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                     Query Match 80.6
Best Local Similarity 84.2
Matches 16; Conservative
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Matches 15; Conservative
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TISSUE=Gall bladder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=45480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          Cynomys
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035225
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                                                                                                                                                                                                                                                                                              Koshino I. Inaba M., Matsumoto M., Ono K.;
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163028; AAD43354.1;
ENSE; PO2730; 1BNX.
INTERPO: IPRO01717; Anion_exchange.
InterPro: IPRO01702; HCO3_cotranspt.
PRINTS: PRO01531; HCO3_cotranspt.
PRINTS: PRO01531; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Bone marrow;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF163826; AAD43593.1; -.

HSSP; P02730; IBNX.

InterPro; IPR001717; Anion_exchange.

InterPro; IPR003102; HCO3_cotranspt.

Pfam; PF00955; HCO3_cotranspt.

Pfam; PF00955; HCO3_cotranspt.

Pfam; PR001231; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                           BKB3.

BKB3.

Bos taurus (Bovine).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.6%; Score 79; DB 6; Length 855;
84.2%; Pred. No. 0.00034;
.ive 1; Mismatches 2; Indels
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
GEQUENCE 930 Aa; 104374 MW; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PKINIS, FINELLE PERCENDER, 1.
TIGREAMS; TICRO0884; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
CPONIENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
                                                                          Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                     855 AA
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                                                          Created)
                     PRT;
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                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
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Best Local Similarity 84.2
Matches 16; Conservative
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                   PRELIMINARY;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                  TISSUE=Kidney
                   09TU00
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Q9XSW5
Q9TUQ0
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                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 103;
Length 930;
                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epithelia.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012895; AAB66833.1;
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
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                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchange protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 52.0 kDa protein (Fragment).
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Pred. No. 0.00035;
0; Mismatches 3;
Score 79; DB 6; Pred. No. 0.00037;
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                                                         Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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TISSUB-Proventriculus;
MEDLINE-96224107; PubMed-8621532;
MEDLINE-96224107; PubMed-8621532;
COX K.H., Adair-Kirk T.L., Cox J.V.;
"Variant AE2 anion exchanger transcripts accumulate in multiple cell
types in the chicken gastric epithelium.";
J. Biol. Chem. 271:8895-8902(1996).
BISSP; PO2730; IBTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                               74.5%; Score 73; DB 4; Length 1159; 83.3%; Pred. No. 0.0044; Live 0; Mismatches 3; Indels
       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;
                                                                                                                                                                                          TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA; 127747 WW; 9F083A2BE8FF5D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                      Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; EC028601; AAH286601.1; InterPro; IPR001717; Anion, exchange. InterPro; IPR003020; HC03_cotranspt. PF009955; HC03_cotranspt.
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Last annotation update)
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Pred. No. 0.0047;
0; Mismatches 3
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InterPro; IPR003005; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORT.
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                                                                                                                                                                                                                                                                                                                                                                        979 SVTHANALTVMSKAVAPG 996
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
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Best Local Similarity
Matches 15; Conserv
                                                      SEQUENCE FROM N.A.
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                     NCBI_TaxID=9606;
                                                                            TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          090710
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090710
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                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to solute carrier family 4, anion exchanger, member 2
(Erythrocyte membrane protein band 3-like 1).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
                                                    74.5%; Score 73; DB 11; Length 466; 83.3%; Pred. No. 0.0017; Live 0; Mismatches 3; Indels
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Pred. No. 0.0023;
0; Mismatches 3; Indels
       1
52003 MW; 481C1108E28D03B1 CRC64;
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                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment)
                                                                                                                                                                                                                                                622 AA.
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InterPro; IPR003020; HCO3_cotranspt.
Prints; PR00355; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                PRT;
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MEDLINE=96339307; PubMed=8756692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry 35:10367-10376(1996)
                                                                                                                                         286 SVTHANALTVMSKAVAPG 303
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                                                                                                                         1 SVTHANALTVMGKASTPG 18
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Local Similarity 83.3%;
les 15; Conservative (
                                                    Query Match 74.5%
Best Local Similarity 83.3%
Matches 15; Conservative
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                                                                                                                                                                                                                                               PRELIMINARY;
                  466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mucosal membranes."
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NON_TER
SEQUENCE
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Best Local 9
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Q9TU75;
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE2 anion exchanger.
SLC4A2.
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Best Local Similarity
Matches 15; Conserv
  HSSP; P02730; 1BTO.
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099654;
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                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                          Medina J.F., Lecanda J., Acin A., Clesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";
Blochem. Biophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF19584.2;
EMBL; U76669; AAF19584.2;
EMBL; U76668; AAF19584.2;
HSSP; P02730; 1BTQ.
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MEDLINE-97179202; PubMed-9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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MEDIJINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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PROSITE; PS00219; ANTON_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1227 AA; 135577 WW; 5D47714C17FB8EF7 CRC64;
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Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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InterPro; IPR003005; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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                  exchanger 2 type bl
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Matches 15; Conservative
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDIINE-97179202; PubMed-9027488;
Medina J.F., Actin A., Prieto J.;
Medina J.F., Actin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 3:74-85(1997).
EMBL; U62531; AAC50964.1; -.
HSSP; P02730; JBYG.
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                                                                                                                                                                                                                          Length 1232;
InterPro; IPRO1717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Plan; PF00955; HCO3_cotranspt.
PR01231; HCO3TRNSPORT.
IIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00229; ANION_EXCHANGER_2; 1.
SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 131019 WW; D266ECDAB238FD97 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                   Score 73; DB 4; Len
Pred. No. 0.0047;
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83.3%; Pred. No. 0.0047;
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                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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InterPro; IPR003020; HCO3_cctranspt.
Pfam; PF00955; HCO3_cctranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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                                                                                                                                                                                                                          74.5%;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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"A structural study of the membrane domain of band 3 by tryptic
digestion. Conformational change of band 3 in situ induced by alkali
treatment.";
J. Biol. Chem. 267:19211-19217(1992).
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"Alternative primary structures in the transmembrane domain of the chicken erythroid anion transporter.";
Mol. Cell. Biol. 8:1327-1335(1988).
EMBL; M19496; AAA48604.1; --
HSSP; P02730; 1BTQ.
Interpro; IPR001717; Anion_exchange.
Interpro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Band 3 protein (Fragments).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13001 MW; E2028D64A8E4A4D1 CRC64;
    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No. 0.0067;
5; Mismatches 1
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66.7%;
                                                               Erythroid anion transporter
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Best Local Similarity 66.7
Matches 12; Conservative
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                                                                                                                                                            NCBI_TaxID=9031;
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NON_TER
SEQUENCE
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Q9UDJ1
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"Band 3, the anion transporter, is conserved during evolution:
implications for aging and vertebrate evolution.";
Cell. Mol. Biol. 41:833-842(1995).
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
NCBI_TaxID-94989;
                                                                                                                                                                             Medina J.F., Lecanda J., Acin A., Clesielczyk P., Prieto J.; "Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene."; Biochem. Biophys. Res. Commun. 267:228-235(2000).
SEQUENCE FROM N.A. MEDLINE-97179202; PubMed-9027488; Medina J.F., Acin A., Prieto J.; Modina J.F., Acin A., Prieto J.; Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene."; Genomics 39:74-85(1997).
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Pred. No. 0.0047;
0; Mismatches 3; Indels
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InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
PROMIS; PF00311; HC03_renspt.
IGRRAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS002202; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 136980 WW; D2FDA72E20D70D64 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAR-2003 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Major anion transport protein band 3 (Fragment)
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EMBL; U76669; ART19583.2; -.
EMBL; U76667; AAF19583.2; JOINED.
EMBL; U76668; AAF19583.2; JOINED.
HSSP; P02730; 1BTQ.
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Matches 14; Conservative
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Query Match

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RESULT 14

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Sequence 39328, A
Sequence 39328, A
Sequence 6, Appli
Sequence 6, Appli
Sequence 1054, A
Sequence 1054, A
Sequence 2, Appli
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156.918 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-087-464-8

US-10-087-464-8

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US-09-920-804-4
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB
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        US-09-734-674-2
        Sequence 2, Appli

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        US-10-274-990-2
        Sequence 3, Appli

        18
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        US-09-738-626-5357
        Sequence 1, Appli

        20
        44
        44.9
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        US-10-087-464-1
        Sequence 1, Appli

        21
        44
        44.9
        272
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        US-09-955-100-1450
        Sequence 1, Appli

        22
        43
        9
        US-09-965-154-2
        Sequence 1, Appli

        23
        42.9
        4551
        11
        US-09-861-289-1
        Sequence 1, Appli

        24
        42.9
        4551
        12
        US-10-166-539-1
        Sequence 1, Appli

        26
        42.9
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        US-10-201-365-2
        Sequence 1, Appli

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        42.9
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        US-10-201-365-2
        Sequence 1, Appli

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        US-09-861-389-6
        Sequence 1, Appli

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                                                                                                                                                                                                                                                                                                                             INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL FOLY30, EVALUE 3.00e-31
INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
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Pred. No. 6.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Stanier, Jonathan S.
APPLICANT: Stanier, Jonathan S.
APPLICANT: Gow, Andrew J.
APPLICANT: Gigel, David J.
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Effects of Hemoglobin
FILE REFERENCE: 1818-1030-003
CURRENT APPLICATION NUMBER: US/10/066,320
CURRENT FILING DATE: 2002-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR PLILORION NUMBER: US60/146,680
PRIOR FILING DATE: 1999-08-02
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELLON NUMBER: US 09/774,203
PRIOR PELLON NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 39328
LENGTH: 86
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Pred. No. 9.7e-08;
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100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVTHANALTVMGKASTPGAA 20
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Publication No. US20030059436Al
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SVTHANALTVMGKASTPGAA 20
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Best Local Similarity luv..
...a 20; Conservative
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US-10-066-320-2
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INFORMATION:
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                                                                                                                                                                                                                     TYPE: PRT
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                                                                                              APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: $1237/7019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENER EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 98; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.8e-09;
Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/087,464 CURRENT FILING DATE: 2002-03-01
                                                                                                                                                                        PRIOR APPLICATION DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SCFWARE: Patentin version 3.0
SEQ ID NO 22
LENTH: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: Aeomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
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PTITING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
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APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 09/632,366
APPLICATION NUMBER: US 09/632,366
FILING DATE: 2000-08-03
FILING DATE: 2000-10-04
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 39328, Application US/09864761 Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SVTHANALTVMGKASTPGAA 20
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              Chishti, Athan
                                                                              Goel, Vikas
                                                      Liu, David
                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-864-761-39328
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Sequence 2, Application US/10260877

Sequence 2, Application US/10260877

Publication No. US20030021813A1

GENERAL INFORMATION:

APPLICANT: Abbort Liands E.

APPLICANT: Hessler, Paul E.

APPLICANT: Hessler, Paul E.

APPLICANT: Hessler, Paul E.

TITLE OF INVENTION: ESSENTIAL BACTERIA GENES AND GENOME

TITLE OF INVENTION: ESSENTIAL GENES.

FILE REFERENCE: 6655.US. PI

CURRENT APPLICATION NUMBER: US/10/260,877

CURRENT APPLICATION NUMBER: US/09/649,145

PRIOR FILING DATE: 2000-08-25

NUMBER OF SEQ ID NOS: 137

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 262

TENGTH: 262
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TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokarvotes
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Mismatches
                                                                            CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2001-12-22

PRIOR FILING DATE: 2001-02-22

PRIOR FILING DATE: 2001-02-22

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SEQ ID NOS: 14110

SEQ ID NO 10954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                       FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 49;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-815-242-10954
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175 SHANFLEVMHKSATKGSA 192
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175 SHANFLEVMHKSATKGSA 192
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Best Local Similarity 55.6'
Matches 10; Conservative
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APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Number: Us, 1002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR PELING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 8
LENGTH: 911
             APPLICANT: Liu, David
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Gool, Vikas
APPLICANT: Li Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S123/77019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
RIGHER APPLICATION NUMBER: US 06/272,930
RIGHER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                              Score 98; DB 15;
Pred. No. 9.7e-08;
; Mismatches 0;
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Pred. No. 9.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10954, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 SVTHANALTVMGKASTPGAA 750
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Best Local Similarity 100.0%; Progress 20; Conservative 0;
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ilarity 100.0%;
Conservative 0;
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Xu, H. Howard
                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Homo sapiens
US-10-087-464-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 20; Conservat
Oh, Steven
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                                                                                                                                                                                                                                                      SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: HC
US-10-087-464-8
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APPLICANT:
APPLICANT:
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APPLICANT:
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Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 44.41
Best Local 8; Conservative
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Pred. No. 22;
4; Mismatches 6; Indels
                                                                   APPLICANT: AUTOLINE ALGUEL ALGUEL APPLICANT: AVIET MATTIN APPLICANT: Xavier Martin APPLICANT: Xavier Martin APPLICANT: Xavier Martin APPLICANT: Steven Charles Jupe APPLICANT: Christopher John Rawlings APPLICANT: Trudy Rachel Doe TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30409-D1 CURRENT FILING DATE: 2000-12-01 PRIOR APPLICATION NUMBER: US/9/728,137 CURRENT FILING DATE: 1998-07-15 PRIOR PELLING DATE: 1998-07-15 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1998-02-09 PRIOR FILING DATE: 1998-02-26
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APPLICANT: XAVIER MAITIN
APPLICANT: Steven Charles Jupe
APPLICANT: Steven Charles Jupe
APPLICANT: Trudy Rachel Doe
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409-D1
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US/99/728,137
CURRENT FILING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1997-07-16
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR PELING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 10
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FastSEQ for Windows Version 3.0
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Best Local Similarity 44.4%;
Matches 8; Conservative
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US-09-728-137-4
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SOFTWARE: FastSEQ for
SEQ ID NO 4
LENGTH: 714
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Sequence 4, Application US/09734674

Facent No. US20020081648A1

GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO1018

CURRENT APPLICATION NUMBER: US/09/734,674

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 1085
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     Length 1032;
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core 47; DB 9;
ed. No. 34;
Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Massian influenced applicant: Aavier Martin APPLICANT: Steven Charles Jupe APPLICANT: Steven Charles Jupe APPLICANT: Christopher John Rawlings APPLICANT: Trudy Rachel Doe TITLE OF INVENTION: NOVEL COMPOUNDS FILE PREPERENCE: GH-30409-D1 CURRENT APPLICATION NUMBER: US/97/28,137 CURRENT FILING DATE: 1996-07-15 PRIOR APPLICATION NUMBER: EP 97401714.7 PRIOR APPLICATION NUMBER: EP 97401713.9 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1997-07-16 PRIOR FILING DATE: 1998-02-09 PRIOR FILING DATE: 1998-02-05 PRIOR FILING DATE: 1998-02
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     Score 47;
Pred. No.
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838 SITHVNSLKLESECSAPG 855
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850 SITHVNSLKLESECSAPG 867
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Search completed: September 3, 2003, 11:53:44 Job time: 18.5 secs
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Publication No. US20030054491A1
GENERAL INFORMATION:
APPLICANT: WEI, MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01018 DIV
CURRENT PEDFLICATION NUMBER: US/10/274,990
CURRENT FILING DATE: 2002-10-22
PRIOR APPLICATION NUMBER: 09/734,674
PRIOR FILING DATE: 2000-12-13
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                                          Gaps
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Patent No. US20020064846Al
GENERAL INFORMATION:
APPLICANT: Sislo, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
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Patent No. US20020064846Al
GENERAL INFORMATION:
APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
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Pred. No. 36;
4; Mismatches 6; Indels
    Length 1085;
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                                        Indels
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  Score 47; DB 9;
Pred. No. 36;
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Pred. No. 36;
                                        Mismatches
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848 SITHVNSLKLESECSAPG 865
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851 SITHVNSLKLESECSAPG 868
                                                                             1 SVTHANALTVMGKASTPG 18
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Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 44.4
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Mus musculus
US-10-274-990-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus US-09-920-804-2
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Gaps
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FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 1088
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851 SITHVNSLKLESECSAPG 868
                                                                                                                                                                                                                                                                         1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                            Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
                                                                                                                TYPE: PRT ORGANISM: Homo sapience US-09-920-804-4
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 3, 2003, 11:42:58; Search time 15.75 Seconds (without alignments) 53.728 Million cell updates/sec Run on:

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 segs, 42310858 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

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/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:* Issued_Patents_AA:'

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	8	7	4	7	7	7	7	7	1,	31,	Θ	465	m	'n	Sequence 3, Appli	3,	7,	•	44,	-	·	9	4		Sequence 5, Appli	523
SUMMAKIES	. TD	US-09-115-954-4	US-09-115-954-8	US-09-115-954-2	US-09-734-674-4	US-09-734-674-2	US-08-926-327-2	US-09-119-918-2	US-09-320-878-1	US-09-141-908-2	US-09-657-440-1	US-09-105-537-31	US-09-105-537-6	US-09-328-352-4650	US-08-491-357-3	US-08-968-633-3	US-09-196-466-3	PCT-US96-10823-3	us-08-700-607-7	US-09-411-977-2	US-07-857-224B-44	US-09-252-991A-19325	us-08-700-607-6	-08-314-	US-08-314-309A-4	US-09-252-991A-23925	US-08-700-607-5	US-09-328-352-5232
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di	Query	48.0	48.0	48.0	48.0	48.0	44.9	44.9	42.9	42.9	42.9	42.9	42.9	40.8	40.8	40.8	40.8	40.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8	39.8
	Score	47	47	47	47	47	44	44	42	42	42	42	42	40	40	40	40	40	39	39	39	39	39	39	39	39	39	39
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Gaps

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48.0%; Score 47; DB 3; Length 714; 44.4%; Pred. No. 7.4; Live 4; Mismatches 6; Indels

Best Local Similarity 44.4%; Matches 8; Conservative

Query Match

APPLICANT: Martin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Tope, Steven C
APPLICANT: Bawlings, Christopher J
APPLICANT: Doe, Trudy R
TILLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH 30409
CURRENT APPLICATION NUMBER: US/09/115,954B

RESULT 2 US-09-115-954-8 Sequence 8, Application US/09115954B ; Patent No. 6200776

GENERAL INFORMATION:
APPLICANT: Boron, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah

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SITHVNSLKLESECSAPG 537 1 SVTHANALTVMGKASTPG 18

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39.8 886 4 US-09-134-001C-4496 Sequence 449 39.3 340 4 US-09-25-991A-27116 Sequence 271 39.3 38.2 US-08-694-915-2 Sequence 271 39.3 416 2 US-08-694-915-2 Sequence 271 39.3 423 4 US-08-25-991A-18849 Sequence 188 38.8 157 4 US-09-252-991A-18849 Sequence 188 38.8 196 5 PCT-US91-09055-5 Sequence 57 38.8 353 4 US-09-252-991A-19956 Sequence 57 38.8 363 4 US-09-252-991A-19956 Sequence 27 38.8 363 4 US-09-252-991A-19956 Sequence 27 38.8 363 4 US-09-252-991A-19956 Sequence 27 38.8 363 4 US-09-252-643-2 Sequence 27 38.8 450 4 US-09-254-667-1 Sequence 17, Sequence 17, Sequence 27,	38.8 452 4 US-09-390-425-2 Sequence 2, pplication US/09115954B 00776 MATION: OCTO, Walter F Til, Antoine M handoudi, Nassirah handoudi, Nassirah cype, Steven C awlings, Christopher J oc, Trudy R ENTION: NOVEL COMPOUNDS CE: GH-30409	CURRENT APPLICATION NUMBER: US/09/115,954B CURRENT FILING DATE: 1998 - 07-15 EARLIER APPLICATION NUMBER: EP97401714.7 EARLIER FILING DATE: 1997-07-16
๛ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ ฺ	38.8  pplicati 0076 MATION: 720, AM AMILIA W AMILIA W AMILIA S EWALINGS EMILIANGS EMIL	ICATION NG DATE: ICATION NG DATE:
A N N N N B B B B B B B B B B B B B B B	38 5-954-4 Co- 4, Ar Co- 62U CANT: BCONT: BCONT: KI CANT: KI CANT: KI CANT: KI CANT: RCONT: KI	NT APPL NT FILTI ER APPL ER FILTI
	RESULT 1 US-09-115-954-4 US-09-115-954-4 Sequence 4 A Patent No. 62 A PAPPLICANT: B APPLICANT: B APPLICANT: A APPLICANT: A APPLICANT: A APPLICANT: A APPLICANT: A APPLICANT: A APPLICANT: B	CURREI CURREI CURREI EARLII EARLIE

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TELEPHONE: 317-276-3334 INFORMATION FOR SEQ ID NO:
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Best Local Similarity 44.4.
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                 RESULT 5
US-09-734-674-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-926-327-2
  US-09-734-674-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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Patent No. 6498022
GENERAL INFORMATION:
APPLICANT: WEL, MING-HUI et al
APPLICANT: WEL, MING-HUI et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO01018
FILE REFERENCE: CL001018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 1085
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11;
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Pred. No. 11;
4; Mismatches
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Pred. No. 12;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BOTON, Walter F
APPLICANT: BATON, Walter F
APPLICANT: Rhandoudi, nassirah
APPLICANT: Khandoudi, nassirah
APPLICANT: Martin, Xavier
APPLICANT: Jupe, Steven C
APPLICANT: Bawlings, Christopher J
APPLICANT: Boe, Trudy R
APPLICANT: Doe, Trudy R
APLICANT: Doe, Trudy R
APLICANT: Doe, Trudy R
APLICANT: DOS, TRUDY R
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT APPLICATION NUMBER: EP97401714.7
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
SEQ ID NO 2
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09115954B Patent No. 6200776
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838 SITHVNSLKLESECSAPG 855
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850 SITHVNSLKLESECSAPG 867
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                                                                                                                                                                                                                                                                                         1 SVTHANALTVMGKASTPG 18
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                                  EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                             Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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Best Local Similarity 44.4%;
Matches 8; Conservative
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                                                                                                                                TYPE: PRT
CRGANISM: Homo sapiens
US-09-115-954-8
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CRGANISM: Homo sapiens
US-09-115-954-2
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                                                                                                                LENGTH: 1032
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GENERAL INFORMATION:
APPLICANT: WEI, MING-Hui et al
APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERBNEE: CLOO1018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT APPLICATION NUMBER: US/09/734,674
SOFTWARE: FASELSQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1129
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                                           Gaps
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  4; Length 1085;
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                                           Indels
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Patent No. 5821100
GENERAL INFORMATION:
APPLICANT: Baltz, Richard H.
TITLE OF INVENTION: Glycosyltransferase Gene gtfB From
TITLE OF INVENTION: Amycolatopsis Orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1.0, Version #1.30
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Pred. No. 13;
  DB
12;
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                                           Mismatches
  Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: P-10898
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-276-3334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/926,32
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                                                                                                                                                                                                                               Sequence 2, Application US/09734674 Patent No. 6498022
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                                                                                                              |:|| |:| : : | ||
848 SITHVNSLKLESECSAPG 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          892 SITHVNSLKLESECSAPG 909
                                                                                  1 SVTHANALTVMGKASTPG 18
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Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
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us-10-087-464-2.rai

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GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: TANG, Li
TILLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
FILE REFERENCE: 300622002100
                                                                                                     APPLICANT: TANG, LIANG, LIANG, LIANG, LIANG, LIANG, LIANG, LIANGENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER PILING DATE: 1998-05-28
EARLIER PILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-05-28
EARLIER FILING DATE: 1998-05-28
NUMBER OF EQ ID NOS: 34
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
LENTH: A551
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Best Local Similarity 56.2%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 6;
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CURRENT PAPLICATION NUMBER: US/09/141,908
CURRENT FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-36
EARLIER FILING DATE: 1998-07-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER APPLICATION NUMBER: PROV. 60/076,919
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1998-03-05
EARLIER FILING DATE: 1908-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Streptomyces venezuelae US-09-320-878-1
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; ORGANISM: Streptomyces venezuelae
US-09-141-908-2
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Patent No. 6503741
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                      Melanie C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                       APPLICANT: McDANIEL, Robert
                                                                                             TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-141-908-2
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                                                                                                                                                   Ouery Match

44.9%; Score 44; DB 2; Length 407;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 10; Conservative 0; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      %305-119-918-2
; Sequence 2, Application US/09119918
; Patent No. 6025173
; GENERAL INFORMATION:
    APPLICANT: Baltz, Richard H.
    APPLICANT: Solenberg, Patricia J.
    TITLE OF INVENTION: Glycosyltransferase Gene gtfB From TITLE OF INVENTION: Amycolatopsis Orientalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 3;
Pred. No. 13;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Webster, Thomas D.
REGISTRATION NUMBER: 39,872
REFERENCE/DOCKET NUMBER: P-10898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/926,327
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-320-878-1; Sequence 1, Application US/09320878A; Patent No. 6117659; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                      371 THARATAVAGTIRTDGAA 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 THARATAVAGTIRTDGAA 388
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TELEPHONE: 317-276-3334
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 55.6%;
Matches 10; Conservative
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SEQUENCE CHARACTERISTICS
                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-09-119-918-2
                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Indiana COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 46285
                                                                                                                  US-08-926-327-2
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1 SVTHANALTVMGKASTPGAA 20
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ORGANISM: Acinetobacter baumannii
US-09-328-352-4650
                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces venezuelae US-09-105-537-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4703 ASASTTAGTAGTPGTA 4718
                                                                                                                                                                                                                                                                                                                                                               Query Match 42.9%;
Best Local Similarity 56.2%;
Matches 9; Conservative
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                                          APPLICANT: Sherman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-328-352-4650
                                                                                                                                                                                                                                                              LENGTH: 11877
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US-08-491-357-3
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                                                                                                                             Sequence 1, Application US/09657440

Patent No. 6509455
GENERAL INFORMATION:
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: BETLACH, Mary C.
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/657,440
CURRENT APPLICATION NUMBER: US/09/657,440
PRIOR APPLICATION NUMBER: US/09-07
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR PILING DATE: 1998-06-29
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN UNIVER: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 4; Length 4.5...
Pred, No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, Y.
APPLICANT: Zhao, Y.
APPLICANT: Shao, Y.
TILLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 31, Application US/09105537A; Patent No. 625520; GENERAL INFORMATION: APPLICANT: Sherman, D.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-105-537-6
; Sequence 6, Application US/09105537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces venezuelae US-09-105-537-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4305 ASASTTAGTAGTPGTA 4320
                     4367 ASASTTAGTAGTPGTA 4382
5 ANALTVMGKASTPGAA 20
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Matches 9; Conserv
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LENGTH: 4613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4551
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Sequence 4650, Application US/09328352

Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
NUMBER OF SEQ ID NOS: 8252
LENGTH: 819
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Patent No. 5716782
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Golemis, Erica A.
APPLICANT: Estolak, Johne
TITLE OF INVENTION: MEDIATOR PROTEIN THAT INDUCES CELLULAR MORPHOLOGICAL
TITLE OF INVENTION: ALTERATIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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APPLICANT: Liu, H.
APPLICANT: Luu, H.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600-438031
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SED: ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
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STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.8%; Score 40; DB 4; I Best Local Similarity 40.0%; Pred. No. 1.4e+02; Matches 8; Conservative 4; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 3;
Pred. No. 1.4e+03;
1; Mismatches 6
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SEQUENCE CHARACTERISTICS:
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Patent No. 6100384
GENERAL INFORMATION:
APPLICANT: Golemis, Erica A.
APPLICANT: Law, Susan
APPLICANT: Estojak, Joanne
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A SIGNAL
TITLE OF INVENTION: ALTERATIONS
TITLE OF INVENTION: ALTERATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1.5e+02;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Dann, Dorfman, Herrell and Skillman
STREET: 1601 Market Street Suite 720
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/968,633
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/491,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-404
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 872 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | |: | :: | | | | 473 STTVAHLLDLVGSASGPG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: not relevant MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 40.8%;
Best Local Similarity 50.0%;
Matches 9; Conservative
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STATE: PA
COUNTRY: USA
... 19103-2307
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US-08-491-357-3
                                                                                                                                                          FILING DATE:
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/ptodata/1/pubpaa/US06_PUBCOMB.pep:
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpaa/PCT_
                                                                                                                                                                                                                                                                                                      513375 segs, 137303645 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                              1 GKASTPGAAQIQEVKEQRI 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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/cgn2_6/
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/cgn2_6/
                                                                                                                                                                             Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                  Sequence:
                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Query Match Length DB ID Description	20 15 US-10-087-464-3 Sequence 3, Appli		ß		. 15		, 10 US-09-963-896-7	15	11 US-09-808-880-3	11 US-09-764-891-3888	10 US-09-738-626-3894	14 US-10-054-562A-4	9 US-09-790-264-39	15 US-10-269-353-39 Sequence 35	
	ength DB I	20 15	42 15	n 6 98	911 15	. 15	. 15	10	15	11	11	10	14	σ		•
ď	Query Match Le	100.0	100.0	100.0	100.0	100.0	100.0	52.1	46.9	45.8	42.7	42.7	42.7	42.7	42.7	
	Score	96	96	96	96	96	96	20	45	44	41	41	41	41	41	
	Result No.	1	7	m	4	Z,	9	7	80	6	10	11	12	13	14	L

Sequence 190, App Sequence 153, Ap Sequence 1364, Ap Sequence 1364, Ap Sequence 2064, Ap Sequence 2064, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 13, Appl Sequence 13, Appl Sequence 1798, Appl Sequence 27, Appl Sequence 3773, Ap Sequence 6639, Appl Sequence 6639, Appl Sequence 6639, Appl Sequence 6639, Appl Sequence 160, Appl Sequence 150, Appl Sequence 160, Appl Sequence 160, Appl Sequence 1781, Appl Sequence 1781, Appl Sequence 1851, Appl Sequence 1851, Appl Sequence 77, Appl Sequence 27, Appl Sequenc
15 US-10-074-475-190 US-10-156-761-753 US-10-156-761-13694 12 US-10-152-300-1450 11 US-09-998-027-1 11 US-09-998-027-1 11 US-09-998-027-1 12 US-10-192-806-12 US-09-988-027-4 US-09-988-200-8 US-09-76-801A-19 US-09-918-201-19 US-09-918-201-19 US-09-918-201-19 US-09-918-201-19 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-14 US-09-918-579-19 US-09-788-626-639 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890 US-09-738-626-6890
1122 1393 1441 1471 11471 11471 1150 1150 1150 1130 1130 1130 1130 113
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| FULLICALION NO. USZUUJUJ9436A1 | GENERAL INFORMATION: | APPLICANT: Chishti, Athar | APPLICANT: Chishti, Athar | APPLICANT: Chishti, Athar | APPLICANT: Chishti, Athar | APPLICANT: Liv, David | APPLICANT: Liv, Xuerong | TITLE NEFERRACE: S123/7019 | CURRENT FILING DATE: 2002-03-01 | PRIOR APPLICATION NUMBER: US/10/087,464 | PRIOR APPLICATION NUMBER: US 06/272,930 | PRIOR FILING DATE: 2001-03-02 | NUMBER OF SEQ ID NOS: 59 | SOFTWARE: Patentin version 3.0 | SEQ ID NO 3 | LENGTH: 20 Length 20; Query Match
100.0%; Score 96; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 20; Conservative 0; Mismatches 0; Sequence 3, Application US/10087464 Publication No. US20030059436A1 ORGANISM: Homo sapiens US-10-087-464-3

ALIGNMENTS

; 0 Indels RESULT 2
US-10-087-464-22
Sequence 22, Application US/10087464
Publication No. US20030059436Al
GENERAL INFORMATION: 1 GKASTPGAAQIQEVKEQRI 20 g δ

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Gaps

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INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.4
INFORMATION: SWISSPROT HIT: P02730, EVALUE 3.00e-21
INFORMATION: EST_HUMAN HIT: BF526005.1, EVALUE 3.00e-21
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Publication No. US2003002267A1
GENERAL INFORMATION:
APPLICANT: Stamler, Jonathan S.
APPLICANT: Stamler, Jonathan S.
APPLICANT: Singel, David J.
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Effects of Hemoglobin
FILE REFERENCE: 1818.1030-003
CURRENT APPLICATION NUMBER: US/10/066,320
CURRENT APPLICATION NUMBER: US/10/066,320
CURRENT APPLICATION NUMBER: US/10/066,320
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastsEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 96; DB 9; Length 86;
Pred. No. 7e-08;
Mismatches 0; Indels
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PELLOR DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 33328
LENGTH: 86
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illarity 100.0%; Pred. No. 1e-06;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens FEATURE:
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US-10-066-320-2
                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MACHER INFORMATION: ED; OTHER INFORMATION: ED;
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Best Local Similarity
Matches 20; Conserv
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                                                                                    APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acom. Ca. X. 1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR PLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
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Pred. No. 3.1e-08;
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PRIOR PELLING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR PLICATION NUMBER: US 09/632,366
PRIOR PAPLICATION NUMBER: GB 24263.6
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39328, Application US/09864761
Patent No. US20020048763A1
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Best Local Similarity 100.0%;
Matches 20; Conservative C
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
                                                   Liu, David
Goel, Vikas
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapien
US-10-087-464-22
                             Steven
                                                                                 APPLICANT
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APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, Second
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
FILE REPERENCE: S1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
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                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BW PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/963,896
FILING DATE: 26-Sep-2001
CILLSIFFCATION: GUKNOWN>
PRIOR APPLICATION: GUKNOWN>
APPLICATION DATA:
APPLICATION NUMBER: 09/397,558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: <Unknown>
ATTORREY/AGBNT IRFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.9%; Score 45; DB 100.0%; Pred. No. 1.6 tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%; Score 50; 60.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFRAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1317 amino acids
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448 GAASSPGSAARLQEL 462
                                                                                                                     COMPUTER READABLE FORM:
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Best Local Similarity 100.
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Best Local Similarity 60.0
Matches 9; Conservative
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APPLICANT: Chishti, Athar
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                                                  APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
APPLICANT: Li, Xuerong
FILE REFERENCE: S1237/7019
FILE REFERENCE: S001-03-03
FILE R
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APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
FILE REFERENCE: S127/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
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Guegler, Karl J.
Corley, Neil C.
TITLE OF INVENTION: PROSTATE GROWTH-ASSOCIATED MEMBRANE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96; DB 15;
Pred. No. 1e-06;
Mismatches 0;
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Patent No. US20020102585Al
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens US-10-087-464-6
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ORGANISM: Homo sapiens
                               Liu, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
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LENGTH: 911
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APPLICANT
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Sequence 4, Application US/10054562A;
Sequence 4, Application US/10054562A;
Publication No. US20020165375A1
GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
TILE OF INVENTION: PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: HW-8-2
CURRENT APPLICATION NUMBER: US/10/054,562A;
CURRENT FILING DATE: 2002-06-10
PRIOR PELLOR DATE: 2001-03-20
PRIOR FILING DATE: 2001-03-20
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.1
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.7%; Score 41; DB 10; Length 345; 50.0%; Pred. No. 1.7e+02; tive 5; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                      APPLICANT: ANIZOGOLII, HINCSHI,
APPLICANT: ANIZOGOLII, HINCSHI,
APPLICANT: HAYASHI, MIKIRO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKHHIRO
APPLICANT: SENOH, AKHHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE REFERENCE: 249-125
CURRENT FILING DATE: 1090-12-18
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SEQ ID NOS: 7059
SEQ ID NO 3894
                                                                                                                                                            Sequence 3894, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Corynebacterium glutamicum US-09-738-626-3894
                                                                                                                                                                                                                               APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGGCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIK'RO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ASTPGAAAQIQEVKEQ 18
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US-10-054-562A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KASTPGAAAQIQ 13
                                            16 QASTPGAALAVO 27
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Best Local Similarity
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/REI: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (88)
. OTHER INFORWATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-891-3888
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                                                                                                                        Sequence 3. Application US/0980880

Fublication No. US2003002728741

GENERAL INFORMATION

APPLICANT: Betlach, Mary C.

APPLICANT: Betlach, Mary C.

APPLICANT: McDaulel, Robert

APPLICANT: Tang, Li

TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE

FILE REPERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/808,880

CURRENT FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/120,24

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-28

PRIOR PLILING DATE: 1999-10-29

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-808-880-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3888, Application US/09764891
; Publication No. US2003007780841
; GENERAL INRORANTION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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1412 SIPGALASLQEVLDQ 1426
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ORGANISM: Artificial Sequence
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Matches 9; Conservative
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12 GKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-764-891-3888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SITE
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08/337,930
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Recipon, Herve
APPLICANT: Chen, Sei-Yu
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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APPLICANT: Macina, Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
US-09-989-920-198
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Best Local Similarity
Matches 6; Conserv
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US-09-989-920-198
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## PATCHER INFORMATION:
## PATCHER INFORMATION:
## PAPLICANT: GoodcarL, Andraw D.J.
## PAPLICANT: GoodcarL, Andraw D.J.
## PAPLICANT: GoodcarL, Andraw D.J.
## PAPLICANT: MCCARTLY, Sean A.
## TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
## TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
## TITLE OF INVENTION: USES
## PRIOR TILING DATE: 1090-04-23
## PRIOR APPLICATION NUMBER: US 09/065,661
## PRIOR APPLICATION NUMBER: US 09/065,661
## PRIOR FILING DATE: 1999-04-23
## PRIOR FILING DATE: 1999-04-23
## PRIOR FILING DATE: 1999-04-23
## PRIOR FILING DATE: 1999-06-22
## PRIOR FILING DATE: 1999-07-29
## PRIOR APPLICATION NUMBER: US 09/124,538
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APPLICANT: HOLIZMANION:
APPLICANT: GOOGGAIL, ANGREW D.J.
APPLICANT: GOOGGAIL, ANGREW D.J.
APPLICANT: GOOGGAIL, ANGREW D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US 10/7269, 353
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: US 09/790, 264
PRIOR FILING DATE: 2001-02-21
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
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     Gaps
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  Indels
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..4e+02;
5;
     4;
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  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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illarity 47.1%; Pred. No. :
Conservative 4: Mismatri
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 39, Application US/10269353 Publication No. US20030104447A1 GENERAL INFORMATION:
                                                                                                                                                                                                                         Sequence 39, Application US/09790264 Patent No. US20020028508A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Drosophila melanogaster
US-09-790-264-39
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292 GAASSPGSAHQSNAIEE 308
                                                 1 GKASTPGAAAQIQEVKEQ 18
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Conservative
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Best Local Similarity
Matches 8; Conserva
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8
Matches
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APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and P
FILE REFERENCE: DEX-0291
CURRENT APPLICATION NUMBER: US/09/989,920
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/252,500
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 284
SOFTWARE: Patentin version 3.1
SEQ ID NO 198
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                                                                                                                                                                                                                                                                                                                                                            Query Match 42.7%; Score 41; DB 15; Length 47 Best Local Similarity 47.1%; Pred. No. 2.4e+02; Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR PILING DATE: 1998-07-29
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1998-07-29
PRIOR PILING DATE: 1998-07-29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
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Job time: 17.5 secs
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40.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 198, Application US/09989920 Patent No. US20020172957A1
                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-269-353-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ||:||:| ::|
292 GAASSPGSAHQSNAIEE 308
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us-10-087-464-3.rai

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Sequence 2083; A Sequence 23893, A Sequence 22380, A Sequence 32336, A Sequence 18394, A Sequence 2, Appli Sequence 32829, A Sequence 31292, A Sequence 28148, A Sequence 29128, A Sequence 29128, A
                                                                                                                                                                                                                                  Sequence 4, Appli
Sequence 27338, A
Sequence 28169, A
Sequence 20548, A
                                                                                                                                                                                 Sequence 29728, A
Sequence 12, Appl
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09083521

Sequence 7, Application US/09083521

Patent No. 6048970

GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Colegler, Karl J.

CONNESSONES TORESSEE: INVERTE PRADABLES:

ADDRESSEE: INVERTE PRADABLE FORM:

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STREET: 34304

COMPUTER: RADABLE FORM:

MEDIUM TYPE: FILPPY disk

COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATE: Herewith

CLASSIFICATION NUMBER: US/09/083,521

FILING DATE: Herewith

CLASSIFICATION NUMBER: PF-0527 US

TELECOMMUTICATION NUMBER: PF-0527 US

TELECOMMUTICATION NUMBER: PF-0527

REFERENCE/DOCKET NUMBER: PF-0527

TELECOMMUTICATION NUMBER: PF-0527

TELECOMMUTICATION NUMBER: PF-0527

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 and ocids

PUBLICATION PORTER NOWED: AND NOWED:
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                             US-09-252-991A-23693
US-09-252-991A-22320
US-09-252-991A-32336
US-09-252-991A-18394
US-09-479-309-2
US-09-677-393-2
US-09-252-991A-31292
US-09-252-991A-31292
                                                                                                                                                             US-09-252-991A-28148
US-09-252-991A-29728
US-09-601-478-1
US-09-601-478-4
US-09-5252-991A-28169
US-09-252-991A-28169
US-09-252-991A-28169
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5; Mismatches
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60.0%; Pred. No.
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Best Local Similarity 60.08
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                 639
704
937
89
239
239
239
330
400
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CLONE: 2459993
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US-09-083-521-7
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Sequence 32531, A
Sequence 22504, A
Sequence 3, Appli
Sequence 24458, A
Sequence 30223, A
Sequence 4, Appli
Sequence 4, Appli
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18921, A
3757, Ap
4, Appli
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Sequence 10, Appl
Sequence 19, Appl
Sequence 30395, R
Sequence 31986, A
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                                                                                                                                (without alignments) 53.728 Million cell updates/sec
                                                                                                              3, 2003, 11:42:58 ; Search time 15.75 Seconds
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Sequence
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-252-911A-32534
US-09-252-911A-22504
US-09-252-911A-31069
US-09-252-991A-3023
US-09-323-421A-4
US-09-812-642-4
US-09-812-642-4
US-09-812-642-4
US-09-812-642-4
US-09-812-642-4
US-09-612-3111
US-09-107-532A-3757
US-09-319-999-4
US-09-412-099A-11
US-09-612-342-11
US-09-612-342-10
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US-09-252-991A-21037
US-09-252-991A-31986
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                                                                                                                                                                                                                                                                                                   328717 segs, 42310858 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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length: 2000000000
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96
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4422.7
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Maximum DB
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Gaps

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Recombinant; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3
                              RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.8%; Score 44; DB 3; 1 60.0%; Pred. No. 2.9e+02;
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Mismatches
                      TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1999-02-16
EARLIER FILING DATE: 1998-10-29
NUMBER: OF SEQ ID NOS: 12
SEQ ID NO 3
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.8%; Score 42; illarity 50.0%; Pred. No. Conservative 3; Mismatcl
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Patent No. 6551795
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; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31069
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1412 SIPGALASLQEVLDQ 1426
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206 TPGAVAQLHGEEEQAV 221
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Best Local Similarity 60.00
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Best Local Similarity
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US-09-252-991A-24458
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Sequence 22504, Application US/09252991A

Sequence 22504, Application US/09252991A

Patent NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC AND THERAPEUTICS

TITLE OF INVENTION: OBJECT: 107106.136

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 22504

LENGTH: 490
                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MAC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32531
LENGTH: 577
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                                                                                                                              Sequence 32531, Application US/09252991A Patent No. 6551795
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Patent No. 6251636
GENERAL INFORMATION:
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32531
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94 GRADQPG-AAEVQQVRRQ 110
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US-09-252-991A-22504
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191 QASTHGADAELQPLREQ 207
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448 GAASSPGSAARLQEL 462
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Best Local Similarity
Matches 9; Conserv
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GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REFERENCE: HW-8
CURRENT APPLICATION NUMBER: 08/09/812,642
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/323,427
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP STREET: P.O. Box 747 CITY: Falls Church STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,286
                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: NAKAWURA, SELJI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: SAKURAI, TONI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
CORRESPONDENCE ADDRESS:
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/08669286 Patent No. 6130060 GENERAL INFORMATION:
                                                                                                                                                                                                             Sequence 4, Application US/09812642 Patent No. 6368600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: MORPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/POCKET NUMBER: 230-
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ. ID. NO: 11:
                                                                                 | |: | ||||:: :|::
283 GAAAKPAAAAQLRLLKKR 300
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                                                       1 GKASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Dirofilaria immitis US-09-812-642-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 44.4%;
Matches 8; Conservative
             8; Conservative
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CLASSIFICATION: 514
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ZIP: 22040-0747
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LENGTH: 387
             Matches
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: MOUSEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30223
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Sequence 4, Application US/09323427

Patent No. 6548329

GENERAL INFORMATION:
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Morales, Tony H.
TITLE OF INVENTION: Parasitic Helminth Cuticlin Proteins, Nucleic Acid
TITLE OF INVENTION: Molecules, and Uses Thereof
FILE REPERENCE: HW-8
CURRENT APPLICATION NUMBER: US/09/323,427

CURRENT FILING DATE: 1999-06-01

EARLIER APPLICATION NUMBER: 60/087,435

EARLIER FILING DATE: 1998-06-01

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0
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Pred. No. 42;
5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 3; Length 387;
Pred. No. 66;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                         2; Mismatches
PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1999-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 24458 LENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30223, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|: || | :: :| ||
98 GRAADPGTGATVRLAEEGRI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24458
                                                                                                                                                                                                                                                                                                                                               218 RAETPGAAALAAAVPOR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30223
                                                                                                                                                                                                                                                                                                     2 KASTPGAAAQIQEVKEQR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 43.8%;
Best Local Similarity 40.0%;
Matches 8; Conservative
                                                                                                                                                                                                          Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Dirofilaria immitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-30223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-427-4
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NAME/KEY: UNSURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
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                                                                                                                                                                  Gaps
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43.8%; Pred. No. 1.6e+02;
tive 5; Mismatches 4; Indels
                                                                                                                            Length 827;
                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09469253

Sequence 11, Application US/09469253

GENERAL INFORMATION:
APPLICANT: NAKAWURA, SEIJI
APPLICANT: SAKURAL, TAKASHI
APPLICANT: NEZU, JUNI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITT: Falls Church
CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/469,253
FILING DATE:
                                                                                                                          Query Match 42.7%; Score 41; DB 3; Best Local Similarity 43.8%; Pred. No. 1.6e+02; Matches 7; Conservative 5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/669,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITUNG DATE:

ATORNEY AGENT
NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 230-110P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/09642146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 827 amirc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                       359 GKTHTVGSVAKVEQVK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 GKTHTVGSVAKVEQVK 374
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amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: protein
US-08-669-286-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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Best Local Similarity
Matches 7; Conserv?
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LENGTH:
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Sequence 18921, Application US/09252991A
Patent No. 6551795
GENERAL INCOMPATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
FRIOR REPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PELICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
GENERAL INFORMATION:
APPLICANT: NAKAMURA, SEIJI
APPLICANT: SAKURAI, TAKASHI
APPLICANT: NEZU, JUNI-ICHI
TITLE OF INVENTION: GENE ENCODING ADSEVERIN
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: BITCH, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/642,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 3;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                            STATE: ...
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230-110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/669,286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MURPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         || | |: |::::||
359 GKTHTVGSVAKVEQVK 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.7%;
Best Local Similarity 43.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GKASTPGAAAQIQEVK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     827 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-09-642-146-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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Search completed: September 3, 2003, 11:52:29
Job time: 17.75 secs
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                                                                                                                                                                                                                                                                                                        Sequence 3757, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLETC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; LOCATION: (252),(292); OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-18921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                  DB 4; Length 460;
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                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.7%; Score 40; DB 4; 36.8%; Pred. No. 30; 1tive 5; Mismatches. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: D. COND. 1303000
COMPUTER: PC
OPERATING SYSTEM: <URNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-507
INFORMATION FOR SEQ ID NO: 3757:
SEQUENCE CHARACTER.ESTICS:
                                                                              ; Score 40.5; DE
; Pred. No. 97;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: USA
ZIP: 02344
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 100 Beaver Street
                                                                                                                                                                                                      193 GRRDAPGASGEVOGEEVEOR 212
                                                                                                                                                                1 GKASTPGAAQIQ-EVKEQR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 137 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 KMSSPGVVPLLDSLKEEKI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7310
                                                                                Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Waltham
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Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                       US-09-107-532A-3757
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                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: HAP3
                                                                                                                                                                                                                                                 Query Match 41.7%; Score 40; DB 3; Length 144; Best Local Similarity 44.4%; Pred. No. 31; Matches 8; Conservative 4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                    ; 9
                                                                                                                                                                                                                                                                                                  | ||: |: || ::||
21 GNASSSGSLQQISTLREQ 38
                                                                                                                                                                                                                                                                                       1 GKASTPGAAAQIQEVKEQ 18
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
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us-10-087-464-4.rapb

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 3, 2003, 11:46:23; Search time 17.5 Seconds Run on:

(without alignments)
156.918 Million cell updates/sec

US-10-087-464-4

112 1 DRILLERPPKYHPDVPYVK 20 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513375 seqs, 137303645 residues Searched:

513375 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

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/cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO8_UBEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USO98_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USO98_PUBCOMB.pep:*

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/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*/cgn2_6/ptodata/1/pubpaa/US10_LNRW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* 'ptodata/1/pubpaa/US10B_PUBCOMB.pep:* cdn2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli	Sequence 23, Appl	Sequence 2, Appli	Sequence 6, Appli	Sequence 8, Appli	Sequence 34894, A	Sequence 1, Appli	Sequence 44, Appl	Sequence 2, Appli	Sequence 4, Appl1	Sequence 2, Appli	Sequence 2, Appli	Sequence 373, App	Sequence 2, Appli	Sequence 176, App
ΙD	US-10-087-464-4	US-10-087-464-23	US-10-066-320-2	US-10-087-464-6	US-10-087-464-8	US-09-864-761-34894	US-09-747-804-1	US-09-908-805B-44	US-09-920-804-2	US-09-920-804-4	US-09-734-674-2	US-10-274-990-2	US-10-205-823-373	US-09-732-020-2	US-09-811-284-176
DB	15	15	15	15	15	σ	σ	10	6	9	σ	15	15	σ	6
% Query Match Length DB	20	51	911	911	911	26	336	542	1088	1088	1129	1129	1035	578	186
% Query Match	100.0	100.0	100.0	100.0	100.0	55.4	46.4	44.6	43.8	43.8	43.8	43.8	42.9	41.1	40.2
Score	112	112	112	112	112	62	52	20	49	49	49	49	48	46	45
Result No.	-	7	3	4	S	9	7	80	6	10	11	12	13	14	15

Sequence 7, Appli Sequence 20, Appl Sequence 20, Appl	Sequence 5, Appli Sequence 570, App Sequence 32, Appl Sequence 33, Appl	Sequence 43138, A Sequence 18, Appl Sequence 18, Appl Sequence 8, Appli	Sequence 8, Appli Sequence 12, Appl Sequence 12, Appl Sequence 16, Appl	Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7, Appli	
12 US-10-177-809-7 10 US-09-965-529-20 11 US-09-969-680A-20 15 US-10-128-714-8075	US-09-842-528- US-10-102-806 US-09-975-143 US-09-975-143	US-09-864-761 US-09-795-926 US-10-364-77 US-09-795-926	12 US-10-364-774-8 9 US-09-795-926-12 12 US-10-364-774-12 9 US-09-795-926-16	US-10-304-774 US-09-795-926- US-10-364-926- US-09-795-926- US-10-364-774 US-09-728-479-	10 US-09-263-689-11 15 US-10-235-674-11. 15 US-10-024-494-4 15 US-10-172-527-16 9 US-09-728-137-4 10 US-09-738-626-5962 11 US-09-919-039-76 9 US-09-728-137-8
360 427 427 641	144 327 47 50	85 97 148	148 186 186 214	265 303 303 324	324 324 393 415 714 920
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4 4 5 4 4 5 7	43.5 43.5 43.5	4 4 4 4 4 3 4 3 4 3 4 3 4 3 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6
16 17 18	55 53 53 53 53 53	25 25 27 27	28 30 31	3 3 3 3 4 3 7 7 4 4 3 7 4 4 5 4 5 4 5 4 5 4 5 4 5 6 6 6 6 6 6 6	30 0 7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

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APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Liu, Nuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
FILE REFERENCE: $1237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 4
SEQ ID NO 5: 59
SET IN NO 4
SEQ ID NO 5: 50
SEQ ID NO 6: 50
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Pred. No. 9e-10;
; Mismatches 0;
Sequence 4, Application US/10087464
Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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Gaps

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Indels

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RESULT 2
US-10-087-464-23
Sequence 23, Application US/10087464
Publication No. US20030059436Al
GENERAL INFORMATION:

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Sequence 34894, Application US/09864761

Patent No. US20020048763a1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Oh, Steven
APPLICANT: Liu, David
APPLICANT: Liu, David
APPLICANT: Gool, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses There
FILE REFERENCE: 51237/7019
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2001-03-02
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4.8e-08;
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Pred. No. 4.8e-08;
; Mismatches 0;
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Pred. No. 4
                      US/10/087,464
                 CURRENT APPLICATION NUMBER: US/10/087,46
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 06/272,930
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
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PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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Matches 20; Conservative
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Best Local Similarity 100.0
Matches 20; Conservative
    REFERENCE: S1237/7019
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SOFTWARE: Patentin versic
SEQ ID NO 8
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US-10-087-464-8
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US-10-087-464-6
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                                                                                                                                                                      LENGTH: 911
TYPE: PRT
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APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
                               APPLICANT: Liu, David
APPLICANT: Goel, Vikas
APPLICANT: Goel, Vikas
APPLICANT: Li, Xuerong
TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
CURRENT APPLICATION NUMBER: US/10/087,464
CURRENT FILING DATE: 2002-03-01
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APPLICANT: Stamler, Jonathan S.
APPLICANT: Stamler, Jonathan S.
APPLICANT: Gow, Andrew J.
TITLE OF INVENTION: Method for Determining Physiological
TITLE OF INVENTION: Effects of Hemoglobin
FILE REFERENCE: 1818.1030-003
CURRENT APPLICATION NUMBER: US/10/066,320
CURRENT APPLICATION NUMBER: PCT/US00/21101
PRIOR PRING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 1999-08-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                       PRIOR APPLICATION NUMBER: 2002-03-01
PRIOR PLING DATE: 2002-03-01
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 59
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 51
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Publication No. US20030059436A1
GENERAL INFORMATION:
APPLICANT: Chishti, Athar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DRILLFKPPKYHPDVPYVK 20
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;
Chishti, Athar
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapien
US-10-087-464-23
                      Steven
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Best Local Similarity
Matches 20; Conserv
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LENGTH: 911
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RESULT 4

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Gaps
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APPLICANT: Seino, Susumu; JCR Pharmaceuticals Co., Ltd.
TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger
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                                                                                                                                                                                                                                                                                                                                                                                      DB 9; Length 336;
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APPLICANT: NICOLA, NICOS A
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
    TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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                        FILE REFERENCE: PF-0576 US
CURRENT APPLICATION NUMBER: US/09/747,804
CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                         Score 52;
Pred. No.
                                                                                         PRIOR APPLICATION NUMBER: 09/131,648
PRIOR FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 44, Application US/09908805B Patent No. US20020147307A1
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RICHARDSON, Rachael
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NICHOLSON, Sandra E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HILTON, Douglas J
APPLICANT: ALEXANDER, Warren S
APPLICANT: VINEY, Elizabeth M
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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US-09-747-804-1
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Matches 9; Conservative
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NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 109762
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US-09-920-804-2
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EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
EXPRESSED IN BT474, SIGNAL = 2.3
EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
EXPRESSED IN HELA, SIGNAL = 1.4
EXPRESSED IN HERA, SIGNAL = 5.1
EXPRESSED IN PRATY, SIGNAL = 5.1
EXPRESSED IN PLACENTA, SIGNAL = 2.2
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0.047;
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                                          PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-10-04
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLILING DATE: 2001-01-30
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Pred. No.
APPLICATION NUMBER: US 09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC009955.1 OTHER INFORMATION: EXPRESSED IN BONE
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Patent No. US20010010913A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RILLLFKPPKYHPDVPYV 19
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Corley, Neil C.
Guegler, Karl J.
Patterson, Chandra
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APPLICANT: Hillman, Jennifer L.
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US-09-864-761-34894
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LENGTH: 56
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APPLICANT:
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Best Local
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APPLICANT:
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APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001018 DIV
CURRENT APPLICATION NUMBER: 02710/22
PRIOR APPLICATION NUMBER: 09/734, 674
PRIOR PRILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                  Sequence 2, Application US/10274990 Publication No. US20030054491A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human
US-10-274-990-2
                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1129
                                              JS-10-274-990-2
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Patent No. US20020001648A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AUGUST THEREOF
FILE REFERENCE: CL001018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US/20020064846A1

GENERAL INFORMATION:

APPLICART: Sealo, Susumu; JCR Pharmaceuticals Co., Ltd.

TITLE OF INVENTION: Sodium Ion-Driven Chloride/Bi-Carbonate Exchanger:

FILE REFERENCE: GP44

CURRENT APPLICATION NUMBER: US/09/920,804

CURRENT FILING DATE: 2001-08-03

NUMBER OF SEQ ID NOS: 8

LENGTH: 1088
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Pred. No. 79;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 9; Length 1088;
Pred. No. 79;
4; Mismatches 7; Indels
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FILE REFERENCE: GP44
CURRENT APPLICATION NUMBER: US/09/920,804
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 2
LENGTH: 1088
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927 DRIKLFWMPAKHQPDFIYLR 946
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| DRIKLFWMPAKHQPDFIYLR 946
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DRIKLEWMPAKHQPDFIYLR 987
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Best Local Similarity 45.0%;
Matches 9; Conservative
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Best Local Similarity 45.0%
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Best Local Similarity 45.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapience
US-09-920-804-4
                                                                                                                               ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-920-804-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Human
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Indels

Score 49; DB 15; Pred. No. 83; 4; Mismatches 7

Length 1129;

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IDENTIFICATION, ASSESSMENT, PREVENTION, AND
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CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR PAPLICATION NUMBER: 60/314,356
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-09-25
PRIOR PELING DATE: 2001-12-12
PRIOR PELING DATE: 2001-12-12
PRIOR PELING DATE: 2001-12-12
PRIOR FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 373, Application US/10205823 publication No. US20030108963A1 GENERAL INFORMATION:
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1 DRILLLFKPPKYHPDVPYVK 20
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Kamatkar, Shubhangi
Wonsey, Angela M.
Glatt, Karen
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Gorbatcheva, Bella
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APPLICANT: Monahan, John E.
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42.9%; Score 48; DB 15; Length 1035;

Query Match

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US-09-811-284-176
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Patent No. US20020058306A1

GENERAL INFORMATION:

TILLE OF INVENTION: No. US20020058306Alel G Protein-Coupled Receptors

FILE REFERENCE: 00167UG1

CURRENT APPLICATION NUMBER: US/09/811,284

CURRENT FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/189,783

PRIOR FILING DATE: 2000-03-16

PRIOR APPLICATION NUMBER: 60/189,917

PRIOR FILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-16
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                                    Gaps
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1.1e+02;
.~c 2; Indels
      Pred. No. 1.1e+02;
4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          N: Human Oxalyl-CoA Decarboxylase
PF119D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 9;
Pred. No. 1.1e+0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-12-08
CURRENT FILING DATE: 2000-12-08
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1997-06-03
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1995-06-03
PRIOR PELICATION NUMBER: 08/458,120
PRIOR PELICATION NUMBER: 08/458,120
PRIOR PELING DATE: 1995-06-02
PRIOR PELING DATE: 1995-06-03
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1995-06-03
PRIOR FILING DATE: 1995-06-03
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1994-05-18
                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09732020
Patent No. US20010003743A1
GENERAL INFORMATION:
APPLICANT: Henrik, Olsen
APPLICANT: Timothy, Coleman
APPLICANT: Mark, Adams
TITLE OF INVENTION: Human Oxalyl-CC
FILE REFERENCE: PF119D3
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FILING DATE: 2000-03-29
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880 DRLKLLLMPLKHQPDFIYLR 899
                                                                                       1 DRILLLFKPPKYHPDVPYVK 20
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Best Local Similarity 45.0%;
Matches 9; Conservative
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292 PPRYQPDVKFIQ 303
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: HOMO SAPIENS
US-09-732-020-2
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SEQ ID NO 2
LENGTH: 578
                                                                                                                                                                                                                                   RESULT 14
US-09-732-020-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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September 3, 2003, 11:42:58; Search time 15.75 Seconds (without alignments) 53.728 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-10-087-464-4 Title: Perfect score:

112 1 DRILLLFKPPKYHPDVPYVK 20 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	Sequence 43, Appl	43,	43,	σ	o	ο	Sequence 15, Appl	À	24,	44,	2,2	æ	Sequence 8, Appli	'n	Sequence 28, Appl	7	7	'n	Sequence 2, Appli	14,	Sequence 14, Appl	14,	Sequence 2, Appli	'n	Sequence 2, Appli	~	Sequence 18, Appl
SUMMAKIES	ID	US-08-405-647B-43	US-08-985-499-43	PCT-US96-03180-43	US-08-405-647B-9	US-08-985-499-9	PCT-US96-03180-9	US-08-269-441A-15	US-09-131-648-1	US-09-012-504A-24	US-09-302-769-44	US-09-734-674-2	US-08-666-367B-8	US-09-143-438-8	US-09-136-652-2	US-08-476-509B-28	US-08-464-342-2	US-08-464-604A-2	US-08-875-272-2	US-08-903-396-2	US-08-405-647B-14	US-08-985-499-14	PCT-US96-03180-14	US-08-458-120-2	US-08-867-970-2	US-09-326-217-2	US-09-732-020-2	US-08-102-385G-18
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	Query Match Length DB	28	28	28	14	14	14	11	336	119	542	1129	376	376	1079	169	147	147	147	147	7	7	7	578	578	578	578	340
æ	Query Match	100.0	100.0	100.0	70.5	70.5	70.5	61.6	46.4	44.6	44.6	43.8	42.9	42.9	42.9	42.4	41.5	41.5	41.5	41.5	41.1	41.1	41.1	41.1	41.1	41.1	41.1	40.2
	Score	112	112	112	79	79	79	69	52	20	20	49	48	48	48	47.5	46.5	46.5	46.5	46.5	46	46	46	46	46	46	46	45
	Result No.	1	7	e	4	2	9	7	<b>&amp;</b>	<u>ه</u>	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 4, Appli Sequence 8, Appli Sequence 8, Appli Sequence 7, Appli Sequence 7, Appli Sequence 12, Appli Sequence 16, Appli Sequence 6, Appli Sequence 11, Appli Sequence 11, Appli Sequence 4, Appli Sequence 14, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli
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1 US-08-446-777-4 1 US-08-446-777-6 2 US-08-446-777-8 1 US-08-446-777-8 4 US-09-795-926-18 4 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-16 5 US-08-46-11 1 US-09-795-926-16 4 US-09-795-926-16 4 US-09-795-926-11 2 US-08-467-94-11 2 US-08-467-94-4 3 US-08-467-94-4 3 US-08-467-94-4 3 US-08-467-94-4 3 US-08-115-954-8 3 US-09-115-954-8
406 767 767 162 97 148 1186 2214 2265 3324 3324 3324 3193 714
44400000000000000000000000000000000000
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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#### ALIGNMENTS

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Sequence 43, Application US/08405647B
Patent No. 6124262
GENERAL INFORMATION:
APPLICANT: Sharman, Irwin W.
APPLICANT: Crandall, Ian E.
APPLICANT: Sholet, Stephen B.
APPLICANT: Thevenin, Bernard Jean-Marie
TITLE OF INVENTION: Compositions and Methods for Reducing
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 112; DB 3; Best Local Similarity 100.0%; Pred. No. 1.1e-10; Matches 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02307E-068700US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/405,647B
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-405-647B-43
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1 DRILLLFKPPKYHPDVPYVK 20

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Gaps

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Indels

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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity.
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US96-03180-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-405-647B-9
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APPLICANT: of California
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                       APPLICANT: Shohet, Stephen B.
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Ilwin
APPLICANT: Sherman, Irwin
ATITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
TITLE OF INVENTION: Mammal
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,499
FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 112; DB 3; 100.0%; Pred. No. 1.1e-10;
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STREET: 201 North Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02307E-084500US
TELECHOME: (415) 576-030
TELEPHONE: (415) 576-0300
TELEPHONE: (415) 576-0300
INFORMATION FOR SED ID NO: 43: SEQUENCE CHARACTERISTICS:
LENGTH: 58 anino acids
TYPE: amino acid
STREE: amino acids
STREET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                   Sequence 43, Application US/08985499
Patent No. 6191103
GENERAL INFORMATION:
APPLICANT: Shohet, Stephen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 DRILLERPPKYHPDVPYVK 27
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DRILLLFKPPKYHPDVPYVK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90012-2628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0
Best Local Similarity 100.3
Matches 20, Conservative
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MOLECULE TYPE: peptide
US-08-985-499-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT-US96-03180-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Ca
COUNTRY:
                                                                                                        RESULT 2
US-08-985-499-43
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APPLICANT: Crandall, Ian E.
APPLICANT: Crandall, Ian E.
APPLICANT: Theorem, Bernard Jean-Marie
APPLICANT: Theorem, Bernard Jean-Marie
TITLE OF INVENTION: Compositions and Methods for Reducing
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 112; DB 5;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                    SOFTWARE: Patenium NUMBER: PCT/US96/03180
FILING DATE:
CLASSIFICATION NUMBER: PCT/US96/03180
FILING DATE:
CLASSIFICATION:
NAME: Berliner, Robert
REGISTATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-370
TELECOMMUNICATION INFORMATION:
TELEFRAX: (213) 977-1001
TELEFRAX: (213) 977-1003
TELEFRAX: (213) 977-1003
SEQUENCE CHARACTERSFICS:
LENGTH: 58 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/405,647B
FILING DATE: 17-MAR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08405647B Patent No. 6124262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRILLLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 DRILLEKPPKYHPDVPYVK 27
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/03180

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Berliner, Robert

REGISTRATION NUMBER: 20,121

REGISTRATION NUMBER: 2555-370

TELEPHONE: (213) 977-1001

TELEPHONE: (213) 977-1003

INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRARCTERISTICS:

LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OURTRANTINGS SISTEM: PC_LOUS/ED. LOUS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/269,441A
FILLING DATE: 30-010-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle Ph.D., Lisa A.
REGISTRATION NUMBER: 07257/009001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 678-5070
TELEFRA: (619) 678-5070
SEQUENCE CHARACTRICS:
SEQUENCE CHARACTRICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rearden, Ann
TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: Los Angeles
STATE: California
COUNTRY: USA
    2: Robbins, Berliner & Carson
201 North Figueroa Street, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/08269441A Patent No. 5552529 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  COUNTRY: USA
ZIP: 90012-7628
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.5%;
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Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 КРРКҮНРБУРУУК 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                        STREET: 201 North
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-269-441A-15
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GENERAL INFORMATION:
APPLICANT: The Regents of the University
APPLICANT: of California
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REDUCING
TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Shohet, Stephen B.
APPLICANT: Sherman, Irwin
APPLICANT: Sherman, Irwin
APPLICANT: von Andrian, Ulrich
TITLE OF INVENTION: Methods for Enhancing Thrombolysis in a
TITLE OF INVENTION: Mammal
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                            Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 14;
                                        Score 79; DB 3; Length 14;
Pred. No. 3.2e-06;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,499
FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.5%; Score 79; DB 3; L
100.0%; Pred. No. 3.2e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Laurence J.
REGISTRATION NUMBER: 35,551
REFERENCE/DOCKET NUMBER: 02307E-084500US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 9:
                                                       100.08; Pro
                                                                                                                                                                                                                                                                                Sequence 9, Application US/08985499 Patent No. 6191103
                    Query Match
Best Local Similarity 100...
Thes 13; Conservative
                                                                                                                                                     1 KPPKYHPDVPYVK 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KPPKYHPDVPYVK 13
                                                                                                                               8 KPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: peptide US-08-985-499-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
US-08-405-647B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-03180-9
                                                                                                                                                                                                                                      RESULT 5
US-08-985-499-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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Gaps

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Length 14; Indels

Gaps

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Length 119;

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NAME/KEY: misc_feature
LOCATION: (103)..(103)
OTHER INFORMATION: The 'Xaa' at location 103 stands for Asp, Gly, Ala, or Val.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STARR, RODYN
APPLICANT: STARR, RODYN
APPLICANT: NICOLGN
APPLICANT: NICOLGN, NICOS A
TILLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC AGENTS
FILE REFERENCE: 109762
CURRENT APPLICATION NUMBER: US/09/302,769
CURRENT APPLICATION NUMBER: 1997-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-10-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 44
                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                 Query Match 44.6%; Score 50; DB Best Local Similarity 53.3%; Pred. No. 1.2; Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50;
Pred. No. 6
                                                                                                    FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)..(662)

OTHER INFORMATION: n=a, c, g, or t

US-09-012-504A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/09302769
Patent No. 6323317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: UNSURE
CATATION: (94)
: OTHER INFORMATION: Xaa is unsure
US-09-302-769-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DRILLLEKPPKYHPDVPYV 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HILTON, Douglas J
APPLICANT: AREXANDER, Warren S
APPLICANT: VINEY, Elizabeth M
APPLICANT: WILLSON, Tracey A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                2 RILLLFKPPKYHPDV 16
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71 RMLFKFEPPLFHPNV 85
      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                        JS-09-302-769-44
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US-09-734-674-2
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                                                                                                                                                                                          Length 11;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-012-504A-24

Sequence 24, Application US/09012504A

Sequence 24, Application US/09012504A

Patent No. 6464974

GENERAL INFORMATION:
APPLICANT: Berlin, V

APPLICANT: Chiu, I.
APPLICANT: Cottarel, G.

APPLICANT: Damagnez, V.

TILE OF INVENTION: IMMUNOSUPRESSANT TARGET PROTEINS
FILE REFERENCE: APPLICATION NUMBER: US/09/012,504A

CURRENT APPLICATION NUMBER: US/09/012,504A

CURRENT FILING DATE: 1994-12-20

PRIOR FILING DATE: 1994-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Exterson, Chandra
TITLE OF INVENTION: EXTRACELULAR ADHESIVE PROTEINS
FILE REFERENCE: PP-0576 US
CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SEQ ID NO : 5
LENGTH: 336
                                                                                                                                                                                        Score 69; DB 1; L
Pred. No. 8.8e-05;
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Pred. No. 1.9;
3; Mismatches
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PRIOR FILING DATE: 1994-05-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                             US-09-131-648-1; Sequence 1, Application US/09131648; Patent No. 6168920
                                                                                                                                                                                                                                 ;
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100.0%;
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llarity 57.1%;
Conservative
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; OTHER INFORMATION: 2635136
US-09-131-648-1
                                                                                                                                                                                        Query Match 61.6
Best Local Similarity 100.
Matches 11; Conservative
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                               1 FKPPKYHPDVP 11
                                                                                                                                                                                                                                                                         7 FKPPKYHPDVP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                    ), NAME/KEY: Peptide
; LOCATION: 1..11
US-08-269-441A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 24
LENGTH: 119
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GENERAL INFORMATION:
APPLICART: WEI, Ming-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REPERENCE: CLO01018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
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                                               Gaps
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Length 542;
                                               Indels
DB 4;
                                             3; Mismatches
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Sequence 8, Application US/09143438 Patent No. 6218161
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   US-09-143-438-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08666367B
Patent No. 5854042
GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION:
PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: 0.C.
COUNTRY: U.S.
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: WG-DOSSIENCE STERM: MS-DOS
SOFTWARE: WG-DOSSIENCE STERM: MS-DOS
SOFTWARE: WG-DOSSIENCE STERM: MS-DOS
SOFTWARE: WG-DOSSIENCE STERM: MS-DOS
SOFTWARE: WG-DOSSIENCE STERM: MS-DOSSIENCE STERM: MS-DO
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NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/666,367B FILING DATE: August 19, 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| | : | |: | |::
968 DRIKLFWMPAKHQPDFIYLR 987
                                                                                                                                                                                                                                                                                                                                                                                                                         1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 45.0%; Pr
Matches 9; Conservative 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:|: | || |:|
223 ILILWDPSVYHADIP 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 53,3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                        ; ORGANISM: Human
US-09-734-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM:
US-08-666-367B-8
                                                                 SEQ ID NO 2
LENGTH: 1129
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US-08-666-367B-8
                                                                                                                                           TYPE: PRT
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RESULT 13

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GENERAL INFORMATION:
APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR TITLE OF INVENTION: PRODUCING THE SAME NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM COMPATIDLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDGPEFFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BRILL, ANTOINE
APPLICANT: KHANDOUDI, NASSIRAH
APPLICANT: MARTIN, XAVIER
APPLICANT: MARTIN, XAVIER
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30010
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT FILING DATE: 1998-08-19
EARLIER APPLICATION NUMBER: EP 974019473.3
EBRILER FILING DATE: 1997-08-19
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
SEQ ID NO 5
SEQ ID NO 5
SEG 
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Pred. No. 9.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/143,438
FILING DATE: August 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-09-136-652-2
Sequence 2, Application US/09136652A
; Partent No. 6096517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/666,367
FILING DATE: August 19, 1996
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08/666,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
FELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 ILLLFKPPKYHPDVP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20006
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PATENT NO. 0.044144

GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY. CHEN
TITLE OF INVESTION: SIGNALLING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVESTION: THEREOF
TITLE OF INVESTION: AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TITLE OF INVESTION: THEREOF
TITLE OF INVESTION: THEREOF
TITLE OF INVESTION: AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICUSES
TOTALE: New Jersey
COMPRESSORE: Klauber & Jackson
STREET: New Jersey
COMPRESSORE: Manuber & Jackson
STREET: New Jersey
COMPRESSORE: Compatible
COMPUTER READABLE FORM:
MEDIUM TYPE: PLONGY MAS.
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATION:
COMPUTER: THE PATENTION DATA:
THING DATE: 01-DEC-1994
CLASSIFICATION NUMBER: 201-DEC-1994
CLASSIFICATION NUMBER: 201-MEN-101 CIP
TELECOMMUNICATION NUMBER: 201-MEN-101
TELECOMMUNICATION: MEN-101
TELECOMMUNICATION: MEN-101
TELECOMMUNICATION: MEN-101
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42.4%; Score 47.5; DB 3; Length 169;
Best Local Similarity 47.6%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 5; Indels
                                                                                                                                          DB 3; Length 1079; 30;
                                                                                                                                                                                                                     7; Indels
                                                                                                                                              Query Match 42.9%; Score 48; DB Best Local Similarity 45.0%; Pred. No. 30; Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-476-509B-28
; Sequence 28, Application US/08476509B
; Patent No. 6034212
                                                                                                                                                                                                                                                                                                                                     924 DREKLELMPEKHQPDFIYER 943
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                                                                                                                                                                                                                                                                                            1 DRILLERPPKYHPDVPYVK 20
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 169 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-476-509B-28
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-136-652-2
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Search completed: September 3, 2003, 11:52:29 Job time: 15.75 secs

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5.1.6
Compugen Ltd.
  version 5 - 2003 (
  GenCore
Copyright (c) 1993
```

OM protein - protein search, using sw model

Run on:

September 3, 2003, 11:41:03; Search time 17.25 Seconds

(without alignments)
111.500 Million cell updates/sec

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:* Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query	y n Length	DB	OI.	Description
	104	1000	1			one the contract of the contra
1 0	104	100.			B3HU	3 anion
ı m	104	100.0	929	7	A25314	3 protei
4	100	96.			150159	יב
5	100	96.2			A30816	band 3 anion trans
9	95	91.3			S59861	3 anion
7	95	Н			S24318	3 anion
æ	93	89.4			A25104	band 3 protein, no
<b>о</b>	93	o	Н		A34911	band 3-related pro
10	93	σ			A31789	band 3-related pro
11	93	o			A56764	band 3-related pro
12	93	89.4	1240		S21086	
13	88	u,			A42497	anion exchanger 3,
14	88	5		•	B34911	band 3-related pro
15	88	ъ.			A33638	erythrocyte anion
16	89				I38496	anion exchanger 3
17	84				S31828	band 3 anion trans
18	53	•			T28858	hypothetical prote
19	48	46.	2 314	7	T44895	probable lipoic ac
20	47	•			T31336	sodium bicarbonate
21	47				T13962	sodium bicarbonate
22	47				T14110	sodium bicarbonate
23	47	٠	٦		PC7034	Na+ bicarbonate co
24	47	•	2 1079		T14031	sodium bicarbonate
25	46	44	П		C72506	hypothetical prote
26	45	43.	3 111		B72722	
27	45	•	m		F69000	cobalamin biosynth
28	45	•	3 727		9	diacylglycerol kin
29	45	43.	3 1119	7	T37460	probable sodium bi

hypothetical prote probable cytochrom	hypothetical prote hypothetical prote NADH2 dehydrogenas	hypothetical prote probable lipoic ac	hypothetical prote PHO85-like protein	u-plasminogen acti cytochrome c-type	hypothetical prote cytochrome c-type	iron binding prote	hypothetical prote	glycine betaine/L-
T22491 H70526	T27828 T27829 T11840	D83699 C70787	T22841 T42379	UKHU E57987	D86101 H91260	T45065	D83563	MMECPW
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1175	1508 1519 115	305	387	431	552 552	332	350	354
43.3	4 4 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	41.3	41.3	41.3	40.9	40.4	40.4	40.4
44	4 4 4 4 4 6	4 4	43	43	42.5	42	42	42
30	3 3 3 3 4 4 5		37 38	39 40	41	43	. 44	45

### ALIGNMENTS

```
Cyaccession: A33810
R; Kudycki, K. E.; Shull, G. E.
J. Biol. Chem. 264, 8185-8192, 1989
A; Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr A; Reference number: A33810; MUID:89255254; PMID:2722777
A; Scatus: preliminary
A; Molecule type: MRNA
A; Residues: 1-848 < KUD>
A; Cross-references: GB:J04793; NID:q203092; PIDN:AAA40800.1; PID:q203093
C; Superfamily: band 3 anion transport protein
C; Keywords: alternative splicing; transmembrane protein
                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
   rat
   transport protein
   anion
band 3
```

Gaps ö Score 104; DB 2; Length 848; Pred. No. 8.3e-09; 0; Mismatches 0; Indels Query Match 100.0%; Best Local Similarity 100.0%; Matches 20; Conservative 0

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657 GMPWLSATTVRSVTHANALT 676 1 GMPWLSATTVRSVTHANALT 20 ŏ a

## RESULT 2

Danid 3 anion transport protein, erythrocyte - human N.Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha C.Species: Homo sapiens (man) 4, anion exchanger, member 1; erythroid anion excha C.Species: Homo sapiens (man) 4, anion 03-0ct-1995 #text_change 22-Jun-1999 C.Accession: A36218; S03074; I39408; I39409; A92237; A26507; A92430; A90323; A28079; R.Lux, S.E.; John, K.M.; Kopitto, R.R.; Lodish, H.F. Proc. Natl. Acad. Sci. U.S.A. 86, 9989-9093, 1989 A; Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange A; Reference number: A36218; MUID:90083213; PMID:2594752

A; Status: preliminary A; Accession: A36218

A; Molecule type: mRNA A; Residues: 1-911 <LUX>

A;Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
R;Tanner, M.J.A.; Martin, P.G.; High, S.
Blochem, J. 256, 703-712, 1988
A;Tille: The complete amino acid sequence of the human erythrocyte membrane anion-tra A;Reference number: S03074; MUID:89134172; PMID:3223947

A; Accession: S03074

A;Molecule type: mRNA A;Residues: 1-55, E',57-911 <TAN> A;Cross-references: EMBL:X12609; NID:928713; PIDN:CAA31128.1; PID:928714 R;Showe, L.C.; Ballanthe, M.; Huebner, K.

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A; Experimental source: erythrocyte
A;Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:1138
A;Note: a histidine residue exsential for anion transport is suggested to be His-651,
B;Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.
J. Biol. Chem. 269, 1918-1926, 1994
A;Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS
A;Reference number: A49717; MUID:94124538; PMID:8294441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A25314
band 3 protein - mouse
CySpecies: Mus musculus (house mouse)
CySpecies: Mus musculus (house mouse)
CySpecies: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
CyAccession: A25314; A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Modecule type: protein
A; Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A; Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857 < CKU>
A; Note: Lys-539 and Lys-851 were shown to bind the same molecule of the anion transpo R; Hamasaki, N: Okubo, K: Kuma, H:; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1997
A; Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fi
A; Reference number: PC4403; MUID:98006310; PMID:9348087
A; Accession: PC4403: MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm
1-403/Region: cytoskeletal protein binding
                                                                                                                                                                                                             A;Status: preliminary
A;Molecule type: protein
A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 361-911 <HAM>
C;Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A
C;Comment: Band 3 has at least two functional domains. Its integral domain mediates
ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
    R;Kang, D.; Okubo, K.; Hamasaki, N.; Kuroda, N.; Shiraki, H.
J. Biol. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. A;Reference number: A44116; WUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 9e-09;
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C; Superfamily: band 3 anion transport protein
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Matches 20; Conserv
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                                                                                                                                              A; Molecule type: DNA
A; Residues: 37-56 <SHO1>
A; Cross references: GB:MI6978; NID:g178217; PIDN:AAA51670.1; PID:g178220
A; Accession: 139409
A; Molecule type: DNA
A; Residues: 118-161.
A; Title: Orlentation of the band 3 polypeptide from human erythrocyte membranes. Identif A; Accession: A92237; MUID:79027186; PMID:701248
A; Accession: A92237; MUID:79027186; PMID:701248
A; Mawby, W.J; Findlay, J.B.C.
Blochem. J; 205, 465-475, 1982
A; Residues: 13 cARIS
A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Recession: A26507
A; Mulcule type: protein
A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Residues: 437-473; 360-369, 248A
A; Releance and C; Mulchy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
B; Raul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H.
A; Residues: 437-473; 360-364, DV, 366-369, CAMA>
A; Reference number: A92430; MUID:83238395; PMID:6345535
A; Reference number: A92430; MUID:83238395; PMID:6345535
A; Accession: A26507
A; And A26507
A; A; Reference number: A92430; MUID:83238395; PMID:6345535
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R; Brock, C.J.; Tanner, M.J.A.; Kempf, C.
Bjochem J. 213, 577-586, 1983
A; Title: The human erythrocyte anion-transport protein.
A; Reference number: A90323; MUID:83308584; PMID:6615451
A; Accession: A90323
A; Mulecule type: protein
A; Residues: 559-630 cas hown to bind phenyl isothicoyanate, an inhibitor of anion transport
A; Node: Lys-590 was shown to bind phenyl isothicoyanate, an inhibitor of anion transport
R; Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
A; Reference number: A28079; MUID:88228050; PMID:3372523
A; Molecule type: protein
A; Reference number: A28079
A; Molecule type: protein
A; Residues: 834-842, XX, 844-911 cKAW>
A; Molecule type: protein
A; Residues: Baya 842, XX, X, 844-911 cKAW>
A; Molecule type: protein
A; Residues: Baya 843, XX, 844-911 cKAW>
A; Molecule type: protein bind the affinity label pyridoxal phosphate, a substrate fc
Biochim Biophys Acter 998, 43-49, 1989
A; Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3
A; Reference number: S05523; MUID:90001294; PMID:2790053
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A; Residues: 361-364, X', 366-372;424-429, 'X', 431-434 <COB>
A; Residues: 361-364, X', 366-372;424-429, 'X', 431-434 <COB>
A; Residues: 361-364, X', 366-372;424-429, 'X', 431-434 <COB>
B; Note: Lys-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Namoukakos, D.; Vasseur, C.; Driancourt, C.; Blouquit, Y.; Delaunay, J.; Wajcman, H.;
Blood 78, 1117-1120, 1991
A; Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of the A; Reference number: A44933; MUID:91329825; PMID:1678289
Genomics 1, 71-76, 1987
A;Title: Localization of the gene for the erythroid anion exchange protein, band 3 (EMPE
A;Reference number: 139408; MUID:88031311; PMID:3478298
A;Accession: 139408
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Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
Reference number: A35835; MUID:91070049; PMID:1701324
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A;Residues: 1-201;20292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 <YANI>
K;Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8283-8290, 1990
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A;Note: sequence extracted from NCBI backbone (NCBIP:49829)
A;Note: sequence of a common polymorphic form designated band 3 Memphis
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Residues: 1.10, 10', 12-68, E', 69-200 <KAU>
Brock, C.J.; Tanner, M.J.A.; Kempf, C.
Lochem. J. 213, 577-586, 1983
FITLE: The human erythrocyte anion-transport protein.
Reference number: A90323; MUID:83308584; PMID:6615451
Accession: A90323
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A; Status: preliminary
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C;Accession: A30816
R;Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816; MUID:89033870; PMID:3185555
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A;Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive
A;Reference number: S24318; MUID:92344566; PMID:1637296
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EMBO J. 14, 5128-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Reference number: S59861; MUID:96080151; PMID:7489705
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A; Cross-references: EMBL:Z50848; NID:g1004316; PIDN:CAA90701.1; PID:g1004317
C; Superfamily: band 3 anion transport protein
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C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C:Accession: S24318, S36083; S22173
B:Huebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.
Biochem. J. 285, 17-23, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          band 3 anion transport protein isoform b - rainbow trout
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 15-Feb_1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
  C;Species: Gallus gallus (chicken)
C;Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
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A;Cross-references: EMBL:X61699; NID:g64308; PIDN:CAA43868.1; PID:g64309
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Pred. No. 4.1e-08;
2; Mismatches 0;
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Pred. No. 2.7e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        band 3 anion transport protein - rainbow trout
                                                                                                                                                                                                                                                  A) Residues: 1-922 <KIM>A) Cross-references: GB:M23404 C; Superfamily: band 3 anion transport protein C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: protein
A; Residues: 71-89;94-114;570-588 <HUE2>
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Best Local Similarity 90.0%;

Matches 18; Conservative
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Best Local Similarity 90.0%;
Matches 18; Conservative 1
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A; Accession: S36083
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A; Accession: S22173
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A; Residues: 1-918 <HUE1>
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A; Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
A; Cross-references: GB:J02756; NID:g192136; PIDN:AAA37278.1; PID:g553874
B; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rovers EMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like pr A; Reference number: A91039; MUID:86274622; PMID:3015590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Accession: 150159
R;Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth
A;Reference number: 150159; MUID:88216609; PMID:2835670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Introns: 5/3; 46/1; 70/3; 131/1; 176/2; 217/3; 245/1; 305/3; 376/1; 447/1; 496/3; 561/
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742 R;Kopito, R.R.; Andersson, M.; Lodish, H.F. J. Biol. Chem. 262, 8035-8040, 1987 A;Title: Structure and organization of the murine band 3 gene. A;Reference number: 149524; MUID:87250387; PMID:3036795
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Kesidues: 1-844 < COS.

A; Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212

C; Superfamily: band 3 anion transport protein
                                                    A; Molecule type: mRNA
A; Residues: 1-929 < KORD>
A; Cross-references: GB: NO577; NID: g49897; PIDN: CAA26506.1; PID: g49898
A; Cross-references: GB: NO577; NID: g49897; PIDN: CAA26506.1; PID: g49898
B; Kopito, R.R.; Lodish, H.F.
J. Cell. Biochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID: 86034211; PMID: 3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 11-466,'S',468-929 <DEM>
A;Cross_references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
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band 3 anion transport protein (clone pBIIIC1) - chicken
A; Reference number: A25314; MUID:85268011; PMID:2410791
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Pred. No. 3.7e-08;
2; Mismatches 0;
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A;Molecule type: DNA'
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A; Residues: 1-929 <KO2>
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C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C; Accession: S21086
R; Gehrig, H.; Mueller, W.; Appelhans, H.
Blochim. Blophys. Acta 1130, 326-328, 1992
A; Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 f A; Reference number: S21086; MUID:92223115; PMID:1562608
                                                               C; Species: Mus musculus (house mouse)
C; Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C; Accession: A31789
R; Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
J; Biol. Chem. 263, 17092-17099, 1988
A; Title: Cloning and characterization of a murine band 3-related cDNA from kidney and A; Reference number: A31789; MUID:89034212; PMID:3182834
A; Accession: A31789
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C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1237 <CHO>
A; Cross-references: GB: 845791; NID: 9256659; PIDN: AAB23488.1; PID: 9256660
A; Experimental source: New Zealand White rabbit, ileal epithelial cells
A; Experimental source: New Zealand White rabbit, ileal epithelial cells
A; Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181)
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A; Residues: 1-1240 <GEH>
A; Cross-references: EMBL: X62137; NID: 928424; PIDN: CAA44067.1; PID: 928425
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-1237 < ALD>
A; Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114
C; Superfamily: Dand 3 anion transport protein
C; Keywords: transmembrane protein
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Pred. No. 7.8e-07;
2; Mismatches 1; Indels
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C;Accession: A56764
K;Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
Am. J. Physiol. 263, 4345-6352, 1992
A;Title: ONA cloning and localization of a band 3-related
A;Reference number: A56764; MUID:93035730; PMID:1415547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB 2; I
Pred. No. 7.8e-07;
2; Mismatches 1;
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Best Local Similarity 85.0
Matches 17; Conservative
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Matches 17; Conservative
                                                         band 3-related protein
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C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C; Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C; Accession: A34911. P.R.; Shull, G.E.
J; Biol. Chem. 265, 462-471, 1990
R; Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J; Biol. Chem. 265, 462-471, 1990
A; Title: CDNA Cloning and tissue distribution of mRNAs for two proteins that are related A; Reference number: A34911. MUD: 90094439; PMID: 2294114
A; Reference number: A34911. MUD: 90094439; PMID: 2294114
A; Residues: 1-1234 < KUUD-A; Residues: GB: J05166; NID: 9203090; PIDN: AAA40799.1; PID: 9203091
A; Cross-references: GB: J05166; NID: 9203090; PIDN: AAA40799.1; PID: 9203090
A; Cross-reference number: A35770; MUD: 90319095; PMID: 2371270
A; Residues: A35770
A; Status: preliminary: nucleic acid sequence not shown; not compared with conceptual tra
A; Molecule type: mRNA
A; Residues: 1-205, A4, 207-924, PG', 927-1017, IV', 1020-1155, ID', 1158-1234 < LIN>
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Homo sapiens (man)
Cispecies: Cispecies: Cispecies (man)
Cispecies: Lansmembrane protein
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Pred. No. 7.8e-07;
Mismatches 1; Indels
                                                                                  Length 918;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 865;
                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                        3 protein, nonerythroid (MEB3) - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 93; DB 2; 1
Pred. No. 5.3e-07;
                                                                               Score 95; DB 2; Pred. No. 2.7e-07;
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                                                                                                                                    1; Mismatches
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C;Superfamily: band 3 anion transport protein C;Keywords: erythrocyte; transmembrane protein
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                                                                                                                                                                                                                 674 GLPWLAAATVRSVTHANALT 693
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90.0%;
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ilarity 85.0%;
Conservative
                                                                               Query Match 91.3
Best Local Similarity 90.0
Matches 18; Conservative
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Best Local Similarity
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Best Local S:
Matches 17,
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Gaps

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Length 1227; 2; Indels

Score 89; DB 2; 1 Pred. No. 3.5e-06; 2; Mismatches 2;

3, 2003, 11:51:16

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erythrocyte anion exchanger homolog AE3 - mouse
C; Species: Mus musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
C; Accession: A33638
R; Kopito, R. R.; Lee, B. S.; Simmons, D. M.; Lindsey, A. E.; Morgans, C. W.; Schneider, K. Cell 59, 927-937, 1989
A; Title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anio A; Reference number: A33638; MUID:90075236; PMID:2686841
A; Reference number: A33638
A; Retaus: preliminary
A; Molecule type: mRNA
A; Rossidues: 1-1227 (KOP)
A; Rossidues: 1-1227 (KOP)
A; Rossidues: 1-1227 (KOP)
C; Superfamily: band 3 anion transport protein
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ilarity 80.0%;
Conservative
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Job time: 18.25 secs
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Best Local Similarity
Matches 16; Conserv
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R;Kudryckl, K.E.; Newman, P.R.; Shull, G.E.
D; Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are related A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rilinn, S.C.; Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 267, 7927-7935, 1992
A;Title: The predicted translation product of a cardiac AE3 mRNA contains an N terminus gene, and identification of an alternative transcription initiation site.
A;Reference number: A42497; MUID:92218461; PMID:1560021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-1030 < LINI>
A; Residues: 1-1030 < LINI>
A; Cross-references: GB:M87060; NID:g202770
A; Cross-references: GB:M87060; NID:g202770
A; Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; this A; Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A; A; A; A; Cross-residues (NCBIN:96971, NCBIP:96975)
A; Molecule type: DNA
A; Residues: 1-73, E' < LINI>
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A.Experimental source: tissue type spleen
C.Superfamily: band 3 anion transport protein
C.Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein
C.Keywords: alternative splicing; cardiac muscle;
                                                                                                                                                                                                                                                                                           anion exchanger 3, cardiac splice form - rat
N'Alternate names: AE3; chloride/bicarbonate exchanger 3
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
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C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
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A;Residues: 1-1227 <KUD>
A;Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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Pred. No. 2.9e-06;
2; Mismatches 2; Indels
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Pred. No. 3.5e-06;
2; Mismatches 2; Indels
                                             Indels
85.0%; Pred. No. 7.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A42497
A; Status: not compared with conceptual translation
                                          2; Mismatches
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Best Local Similarity 80.0%;
Matches 16; Conservative 2
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               Best Local Similarity 85.0% Matches 17; Conservative
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Best Local Similarity 80.09
Matches 16; Conservative
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RESULT 15 A33638

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version 5.1.6 - 2003 Compugen Ltd.
  GenCore
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OM protein - protein search, using sw model

September 3, 2003, 11:41:03; Search time 17.25 Seconds Run on:

(without alignments)
111.500 Million cell updates/sec

US-10-087-464-4 112 1 DRILLLFKPPKYHPDVPYVK 20 Title: Perfect score:

Sequence:

BLOSUM62 Gapon 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	band 3 anion trans	3 anion	band 3 protein - m	c t	band 3 anion trans		3-	3-related	band 3-related pro	anion exchange pro	anion exchanger 3,	band 3-related pro	erythrocyte anion	probable sodium bi	hypothetical prote	sodium bicarbonate	anion exchanger 3	acid phosphatase (	band 3 anion trans	3 anion tra	BGLF2 protein - hu		acid phosphatase (	Na+ bicarbonate co	probable histone d	hypothetical prote	methylaspartate am	sporulation specif	sodium bicarbonate
SUMMARIES	qī	взни	A33810	A25314	150159	A30816 .	A25104	A34911	A31789	A56764	S21086	A42497	B34911	A33638	T37460	T22491	T31336	I38496	B84540	S59861	S24318	QQBE40	H84669	A59200	PC7034	B75095	H71071	T43810	C96940	T13962
	BB	-1	7	7	7	7	7	7	~	~	~	7	~	~	~	7	~	~	-	7	7	-	Н		7	7	_	7	N	7
	Query Match Length	911	848									1030	1227	1227	1119	1175	1035	1232	468	912	918	336	469	473	1079	.334	332	413	605	1035
ď	Query Match	100.0	96.4	96.4	73.2	73.2	66.1	66.1	66.1	66.1	66.1	60.7	60.7	60.7	58.9	58.9	56.2	55.4	44.6	44.6	44.6	43.8	43.8	43.8	43.8	42.9	42.9	42.9	42.9	42.9
	Score	112	108	108	82	82	74	74	74	74	74	68	68	89	99	99	63	62	20	20	20	49	49	49	49	48	48	48	48	48
	Result No.	г	7	6	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

sodium bicarbonate	sodium bicarbonate	conserved hypothet	transglutaminase t	acid phosphatase (	acid phosphatase (	hypothetical prote	hypothetical prote	replicative DNA he	hypothetical prote	hypothetical prote	alpha 2,6-sialyltr	beta-galactoside a	beta-galactoside a	acid phosphatase (	nodule-specific hy
T14110	T14031 ·	F69019	B84146	T04599	F96605	T30143	E72237	G82329	T23748	AH1642	C42327	A28451	A41734	A59201	S11967
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1035	1079	234	284	466	466	137	306	468	1156	77	214	403	406	431	434
42.9	42.9	42.0	42.0	42.0	42.0	41.1	41.1	41.1	41.1	40.6	40.2	40.2	40.2	40.2	40.2
48	48	47	47	47	47	46	46	46	46	45.5	45	45	45	45	45
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999
C; Accession: A36218; S03074; I39409; A92237; A26507; A92430; A90323; A28079;
R; Lux, S.E.; John, K.M.; Kopito, R.R.; Lodish, H.F.
Proc. Natl. Acad. Sci. U.S.A. 86, 9089-9093, 1989
A; Title: Cloning and characterization of band 3, the human erythrocyte anion-exchange A; Accession: A36218; MUID:90083213; PMID:2594752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-911 cLUX>
A; Residues: 1-911 cLUX>
A; Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
A; Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
B; Tanner, M.J.A.; Martin, P.G.; High, S.
Biochem J. 256, 703-712, 1988
A; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra
A; Reference number: S03074; MUID:89134172; PMID:3223947
band 3 anion transport protein, erythrocyte - human
N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion excha
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A; Molecule type: mRNA A; Residues: 1-55, E', E', 57-911 <TAN> A; Cross-references: EMBL:X12609; NID:928713; PIDN:CAA31128.1; PID:928714 A; Cross-references: Ballantine, M.; Huebner, K. Genomics 1, 71-76, 1987 A; Title: Localization of the gene for the erythroid anion exchange protein, band 3 (E A; Reference number: 139408; MUID:88031311; PMID:3478298

A, Accession: 139409 A; Molecule type: DNA A, Residues: 118-161 <SHO2> A; Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169 R; Drickamer, L.K. A;Molecule type: DNA A;Residues: 37-56 <SHO1> A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220

A; Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden A; Reference number: A92237; MUID:79027186; PMID:701248

A;Accession: A92237
A;Molecule type: protein
A;Residues: 1-3 <DRI>
B;Mawby, W.J.; Findlay, J.B.C.
Biochem. J. 205, 465-475, 1982
A;Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-A;Reference number: A26507; MUID:83074521; PMID:7150226

A;Molecule type: protein A;Residues: 437-473;806-364,'D',366-369 <WAN> R;Kaul, R.K.; Murthy, S.N.P.; Reddy, A.G.; Steck, T.L.; Kohler, H. J. Biol. Chem. 258, 7981-7990, 1983

A; Accession: A26507

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A33810
band 3 anion transport protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
C;Accession: 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr
A;Reference number: A33810; MUID:89255254; PMID:2722777
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C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A25314, A26086; 149524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                                                                      A;Map position: 17q21-17q22
C;Superfanily: band 3 anion transport protein
C;Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm
F;1-403/Region: cytoskeletal protein binding
                   C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093 C;Superfamily: band 3 anion transport protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           experimental
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F;539,590,851/Binding site: anion (Lys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TM08>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Keywords: alternative splicing; transmembrane protein
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100.0%; Pred. No. 5.5e-09;
ive 0; Mismatches 0;
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Pred. No. 2.1e-08;
1; Mismatches 0
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                                                                                                                                                                                                                                          F;404-91.77. cy coskeletal protein bin. F;404-417. Region: anion antiporter F;405-427. Domain: transmembrane #status F;435-457. Domain: transmembrane
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Matches 19; Conservative
                                                                                                    A; Gene: GDB: SLC4A1; EPB3
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Matches 20; Conserv
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A; Residues: 1-848 <KUD>
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F;491-507/Domain:
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ANTILLS INTO acid sequence of the Nullpha) terminal 301 residues of human erythrocyte Anteceasion, 50240
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R.Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Biol. 8, 4416-4442 4, 1988
Mol. Cell. Biol. 9, 4416-4442 4, 1988
A.Title: Two different mRNAs are transcribed from a single genomic locus encoding the A; Reference number: A30816; MUID:89039870; PMID:3185555
A; Accession: A30816
A; Molecule type: mRNA
A; Residues: 1-922 < KINS
A; Residues: 1-922 < KINS
A; Cross-references: GB:M23404
C; Superfamilly: band 3 anion transport protein
C; Keywords: transmembrane protein
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A. Residues: 1-1234 (KUD)
A. Cross references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A. Cross references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
R. Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990
A. ATHILE: Functional expression and subcellular localization of an anion exchanger clo
A. Reference number: A35770; MUID:90319095; PMID:2371270
A. Stetues: preliminary; nucleic acid sequence not shown; not compared with conceptual
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-205, A', 207-924, PG', 927-1017, IV', 1020-1155, ID', 1158-1234 <LIN>
C; Superfamily: band 3 anion transport protein
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R; Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rov EMBO J. 5, 1205-1214, 1205-1214, A; Title: Cloning and structural characterization of a human non-erythroid band 3-like A; Reference number: A91039; MUID:86274622; PMID:3015590
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C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A35770
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rela
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C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
                                              C; Date: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
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C,Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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band 3 protein, nonerythroid (MEB3) - human (fragment)
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Pred. No. 0.0034;
3; Mismatches 4;
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761 ERLHLLLMPPKHHPDVTYVK 780
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    C; Species: Gallus gallus (chicken)
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Best Local Similarity 65.0%;
Matches 13; Conservative
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A; Molecule type: mRNA
A; Residues: 1-865 < DEM>
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A; Status: preliminary
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A:Molecule type: DNA
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C, Species: Gallus gallus (chicken)
C, Species: Gallus gallus (chicken)
C, Date: 13-Sep-1996 #Sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C, Accession: 150159
R; Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A; Title: Alternative primary structures in the transmembrane domain of the chicken eryth A; Reference number: 150159; MUD: 88216609; PMID: 2835670
A; Accession: 150159
A; Status: preliminary; translated from GB/EMBL/DDBJ
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C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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A; Residues: 1-929 <KO2>
A; Residues: 1-929 <KO2>
A; Cross-references: GB-N2379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B; Kopito, R.R.; Andersson, M.; Lodish, H.F.
J. Biol. Chem. 262, 8035-8040, 1987
A; Title: Structure and organization of the murine band 3 gene.
A; Reference number: 149524; MUID:87250387; PMID:3036795
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A;Residues: 1-844 <COX>
A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
                            A Accession: A2514
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-929 < KKOP>
A; Cross-references: GB:X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898
B; Kopito, R.R.; Lodish, H.F.
Cell Blochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MUID:86034211; PMID:3840489
A; Accession: A26086
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A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:g53042; PIDN:CAA27555.1; PID:g53043
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Pred. No. 0.0002;
0; Mismatches 4; Indels
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A30816
band 3 anion transport protein (clone pBIIIC1) - chicken
A; Reference number: A25314; MUID:85268011; PMID:2410791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 DRILLLFKPPKYHPDVPFVK 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DRILLLFKPPKYHPDVPYVK 20
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Best Local Similarity 78.9%;
Matches 15; Conservative
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C;Accession: B34911
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
T. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are rela A;Reference number: A34911; MUID:90094439; PMID:2234114
A;Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anion exchanger 3, cardiac splice form - rat
N;Alternate names: AE3; chloride/bicarbonate exchanger 3
C;Species: Ratus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
C;Accession: A42497; B42497
S.Lin S.C.; Kudryck, K.E.; Shull, G.E.
A;Fitle: The predicted translation product of a cardiac AE3 mRNA contains an N termin gene, and identification of an alternative transcription initiation site.
A;Reference number: A42497; MUID:92218461; PMID:1560021
A;Accession: A42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M87060; NID:g202770
A;Note: this translation is not annotated in GenBank entry RATAE3A, release 111.0; th
A;Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
Complete nucleotide sequence of band 3 related anion transport protein AE2 nce number: S21086; MUID:92223115; PMID:1562608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             port protein cardiac muscle; heart; transmembrane protein
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                         A;Cross-references: EMBL:X62137; NID:928424; PIDN:CAA44067.1; PID:928425 C;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771
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Pred. No. 0.034;
4; Mismatches
                                                                                                                                                                                                                                                                                           DB 2;
0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                        Score 74; DB 2
Pred. No. 0.005
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: tissue type spleen C; Superfamily: band 3 anion transport prot C; Keywords: alternative splicing; cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
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928 RLLLIFMPAKHHPEQPYV 945
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                                                                                                                                                                                                                                                                                           66.1%;
65.0%;
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61.1%;
                                                                                                                                                                                                                                                                                           Query Match 66.1
Best Local Similarity 65.0
Matches 13; Conservative
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Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-73, 'E' <LIN2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-1030 <LIN1>
                                                                                    A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1240 <GEH>
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A; Residues: 1-1227 <KUD>
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                                                         A; Accession: S21086
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                                                                                                                                                                                                                                                                                                                                                                       Dand 3-related protein - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Ja. May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
C; Accession: A31789
R; Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
J. Biol. Chem. 263, 17092-17099, 1988
A; Title: Cloning and characterization of a murine band 3-related cDNA from kidney and fr. A; Reference number: A31789; MUD:89034212; PMID:3182834
A; Accession: A31789
A; Residues: 1-1237 < ALP>
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         band 3-related protein, ileum - rabbit
band 3-related protein, ileum - rabbit
band 3-related protein, ileum - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: O8-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C;Accession: A56764
Mm. J. Physiol. 263, G345-G352, 1992
A;Title: cDNA cloning and localization of a band 3-related protein from ileum.
A;Reference number: A56764
A;Stetus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1237 cCHO>
A;Gross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660
A;Gross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660
A;Experimental source: New Zealand White rabbit, ileal epithelial cells
A;Note: sequence extracted from NCBI backbone (NCBIN:I15180, NCBIP:I15181)
C;Superfamily: band 3 anion transport protein
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anion exchange protein 2 - human
cispecies: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S21086
E;Gehrig, H.; Mueller, W.; Appelhans, H.
Biochim. Biophys. Acta 1130, 326-328, 1992
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                                                            Length 1234;
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                                                                                                                  4; Indels
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1larity 65.0%; Pred. No. 0.005;
Conservative 3; Mismatches
                                                            DB 2;
                                                                                       0.005;
                                                                                                               3; Mismatches
                                                            Score 74;
Pred. No.
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1133 ERLHLLLMPPKHHPDVTYVK 1152
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1133 ERLHLLLMPPKHHPDVTYVK 1152
                                                                                                                                                                               1 DRILLERPPKYHPDVPYVK 20
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   C; Keywords: transmembrane protein
                                                            66.1%;
65.0%;
                                                                                                                     13; Conservative
                                                                                       Best Local Similarity
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es 13; Conserv
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ses 13; Conserv
                                                            Query Match
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Gaps

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Length 1175; Indels

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Moleocule type: DNA
A;Residues: 1-1175 <WILL>
A;Cross-references: EMBL:Z75541; PIDN:CAA99853.1; GSPDB:GN00019; CESP:F52B5.1
                                                                                                                                                                                                                                                                               A;Map position: 1
A;Introns: 67/1; 156/1; 190/3; 253/3; 636/1; 757/3; 977/3; 1021/3; 1139/3
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.9%; Score 66; DB 2; Best Local Similarity 60.0%; Pred. No. 0.079; Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: September 3, 2003, 11:51:20 Job time: 18.25 secs
                    submitted to the EMBL Data Library, June 1996
A;Reference number: 219570
A;Accession: T22491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                      A, Experimental source: clone F52B5 C, Genetics:
                                                                                                                                                                                                                                                          A; Gene: CESP: F52B5.1
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R;Romero, M.F.; Boron, W.F.
submitted to the EMBL Data Library, May 1997
A;Description: Identification of a C. elegans protein similar to the electrogenic Na/HCC
A;Reference number: 221700
A;Accession: T37460
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                       erythrocyte anion exchanger homolog AE3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: O2-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
C;Accession: A33638
R;Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K.
A;Title: Regulation of intracellular PH by a neuronal homolog of the erythrocyte anion A;Reference number: A33638; WUID:90075236; PMID:2686841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable sodium bicarbonate cotransport protein NBC - Caenorhabditis elegans
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C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
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                                                         Gaps
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A;Molecule type: mRNA
A;Residues: 1-1227 <KOP>
A;Cross-references: GB:M28383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C;Superfamily: band 3 anion transport protein
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Score 68; DB 2; Length 1227; Pred. No. 0.041;
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Pred. No. 0.075;
2; Mismatches 6; Indels
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Pred. No. 0.041;
4; Mismatches
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C; Genetics:
                                                 4; Mismatches
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1125 RLLIFWPAKHPEQPYV 1142
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1125 RLLLIFMPAKHHPEQPYV 1142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RILLLFKPPKYHPDVPYV 19
Match 60.7%;
Local Similarity 61.1%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.7%;
Best Local Similarity 61.1%;
Matches 11; Conservative
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Best Local Similarity 60.0%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-1119 <ROM>
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Query Match
Best Local S
Matches 11
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 3, 2003, 11:41:03; Search time 17.25 Seconds Run on:

(without alignments)
111.500 Million cell updates/sec

US-10-087-464-2 98 1 SVTHANALIVMGKASTPGAA 20 Perfect score:

Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 Total number of hits satisfying chosen parameters: 283308 segs, 96168682 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	band 3 anion trans	band 3 anion trans	m	band 3 protein, no	band 3-related pro	band 3-related pro	band 3-related pro	anion exchange pro		band 3 anion trans	band 3 anion trans	band 3 anion trans	anion exchanger 3,	band 3-related pro	erythrocyte anion	anion exchanger 3	band 3 anion trans	hypothetical prote	hypothetical prote		outer membrane pro	proline dehydrogen	transferase homolo	nucleolin - human	cell division prot	probable transcrip	basic leucine zipp	hypothetical prote	
· SUMMARIES	QI	взни	A33810	A25314	A25104	A34911	A31789	A56764	S21086	I50159	A30816	S59861	S24318	A42497	B34911	A33638	I38496	S31828	164139	E97835	н95911	S07575	T28435	T30585	A35804	B71638	E95911	T09120	T19835	T47801
	DB	1	~	7	~	~	~	a	~	7	~	~	7	~	~	7	~	~	7	~	7	~	7	7	7	7	7	7	7	~
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ď	Query Match	100.0	92.9	92.9	74.5	74.5	74.5	74.5	74.5	72.4	72.4	64.3	64.3	62.2	62.2	62.2	62.2	58.2	50.0	49.0	48.5	48.0	45.9	44.9	43.4	42.9	42.9	42.9	42.9	42.9
	Score	86	91	91	73	73	73	73	73	71	71	63	63	61	61	61	61	57	49	48	47.5	47	45	44	42.5	42	42	42	42	42
	Result No.	-	7	m	4	5	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

polyketide synthas	hypothetical prote	orfl 5' to fcc - S	triosephosphate is	triosephosphate is	geranylgeranyl dip	ABC transporter, s	probable solute-bi	probable nucleic a	probable RTX famil	hypothetical prote	latent transformin	translation initia	hypothetical prote	hypothetical prote	methionine.aminope	
T17409	T12541	A44238	AH2775	F97555	C75400	AG2724	C97506	H75272	B85547	F90696	A55494	AE3544	A82459	T37094	B87106	
N	N	~	7	~	7	7	7	~	7	7	7	7	7	7	7	
4613	430	122	256	256	329	497	509	603	5188	5291	1820	128	144	206	285	
6.	٣.	ω.	œ.	ω.	ω.	ω.	۰	ω.	æ.	41.8	m.	ω.	ω.	8.	ω.	
42	42	41	41	41	4.1	41	41	41	41	41	41	40	40	40	40	
42	41.5	41	41	41	41	41	41	41	41	41	40.5	40	40	40	40	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

#### ALIGNMENTS

RESULT 1 Bald  Band 3 anion transport protein, erythrocyte - human  Bald  Band 3 anion transport protein, erythrocyte - human  Bald  Band 3 anion transport protein, erythrocyte - human  Bald  Bald  Cibate: 03-Aug-1984 #sequence_revision 03-Oct-1995 #text_change 22-Jun-1999  Cibate: 03-Aug-1984 #sequence of band 3, the human erythrocyte anion-exchange A; Restitues: preliminary  A; Restitues: preliminary  A; Status: preliminary  A; Status: preliminary  A; Status: preliminary  A; Status: preliminary  A; Cross-references: GB:M27819; NID:g178215; PIDN:AAA35514.1; PID:g178216  B; Pand: A; Martin, PG; High, S.  Biochem. J. 255, 703-712, 1988  A; Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra  A; Restitues: 1-55, 703-712, 1988  A; Molecule type: mRNA  A; Restitues: 1-55, E', ST-911 < TANN  A; Restitues: 1-55, E', ST-911 < TANN  A; Restitues: 1-55, E', ST-911 < TANN  Bald  Ba
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Genomics 1, 71-70, 1987 Affilte: Localization of the gene for the erythroid anion exchange protein, band 3 (E A;Reference number: 139408; MUID:88031311; PMID:3478298 A;Accession: 139408

A; Roceule type: DNA
A; Residues: 37-56 <SHO1>
A; Accession: 139409
A; Accession: 139409
A; Accession: 139409
A; Accession: 139409
A; Residues: 181-161
A; Accession: 139409
A; Residues: 181-161
A; Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g178220
A; Residues: 181-161
A; Cross-references: GB:M16979; NID:g178218; PIDN:AAA51671.1; PID:g553169
B; Drickamer, L.K.
A; Title: Orientation of the band 3 polypeptide from human erythrocyte membranes. Iden
A; Reference number: A92237; MUID:79027186; PMID:701248
A; Accession: A92237
A; Molecule type: Drotein
A; Residues: 1-3 <CRN
A; Mawby, W.J; Findlay, J.B.C.
B; Maccession: A26507; MUID:83074521; PMID:7150226
A; Title: Characterization and partial sequence of di-iodosulphophenyl isothiocyanate-A; Reference number: A26507; MUID:83074521; PMID:7150226
A; Accession: A26507; MUID:83074521; PMID:7150226

A;Molecule type: protein A;Residues: 437-473;580-364,'D',366-369 <MAW> R;Reul, R.K.; Murthy, S.N. P.; Reddy, A.G.; Steck, T.L.; Kohler, H. J. Biol. Chem. 258, 7981-7990, 1983

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C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site: anion (Lys)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                transmembrane #status
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nes 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F:459-479/Domain:
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A; Mesidues: 1-55, Fz. 57-69 <TANN2>
A; Residues: 1-55, Fz. 57-69
A; Note: sequence extracted from NCBI backbone (NCBIP:49829)
A; Note: sequence of a common polymorphic form designated band 3 Memphis
B; Kang, D; Okubo, K; Hamasaki, N; Kuroda, N; Shiraki, H.
A; Biol. Chem. 267, 19211-19217, 1992
A; Title: A structural study of the membrane domain of band 3 by tryptic digestion. Confc
A; Reference number: A44116; MUID:92406862; PMID:1527044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Molecule type: protein

A. Molecule type: protein

A. Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 < KAN

A. Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 < KAN

A. Residue to service extracted from NCBI backbone (NCBIP:113819, NCBIP:113821, NCBIP:113823, A. Note: a histidine residue essential for anion transport is suggested to be His-651, Hi

R. Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.

J. Biol. Chem. 269, 1918-1926, 1994

A. Feference number: A49717; MUID:94124538; PMID:8294441

A. Accession: A49717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: 559 (30 c8R0)
A; Molecule type-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport R; Kawano, Y.; Okubo, K.; Tokunaga, F.; Miyata, T.; Iwanaga, S.; Hamasaki, N.
B Bol. Chem. 263, 832-838, 1988
A; Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal region A; Reference number: A28079; MUID:88228050; PMID:3372523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 361-364, X', 366-372;424-429, X', 431-434 <COB>
A; Residues: 361-364, X', 366-372;424-429, X', 431-434 <COB>
A; Note: Lyps-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Note: Lyps-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Note: Lyps-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
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B; Note: Lyps-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Note: Lyps-430 is labeled by eosinyl-5-maleimide (EMA) in intact erythrocytes
B; Note: Lyps-430 is labeled by eos
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A; Residues: 361-911 <HAM>
C; Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
A; Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A; Reference number: A92430; MUID:83238395; PMID:6345535 A; Accession: A93430 A; Accession: A92430 A; Accession: A90323
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A; Residues: 1-701;220-292;307-308,'R',310-312,'S',314-329,'K',331-333;347-370 < YAN1>
R; Cobb, C.E.; Beth, A.H.
Biochemistry 29, 8288-8290, 1990
A; Title: Identification of the eosinyl-5-maleimide reaction site on the human erythrocyt
A; Reference number: A35835; MUID:91070049; PMID:1701324
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A;Title: Proteclytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel
A;Reference number: PC4403; MUID:98006310; PMID:9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <OKU>
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A; Realdues: 834-842, "x, 044-911 < RAW>
A; Realdues: 834-842, "x, 044-911 < RAW>
A; Roteldues: B34-842, "x, 044-911 < RAW>
A; Roteldues: B34-854, "x, 044-911 < RAW>
A; Vote: Lys-851 was shown to bind the affinity label pyridoxal phosphate, a substrate f R; Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Wajcman, H.
Blochim: Blophyys. Acte 998, 43-49, 1989
A; Yitle: Primary structure of the cytoplasmic domain of human erythrocyte protein band A; Reference number: S05523; WUID:90001294; PMID:2790053
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A;Accession: A44933
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A; Residues: 427-436;479-519;538-540;559-566;809-817;825-841;849-857
A; Note: Lys-539 and Lys-851 were shown to bind the same molecule of
B; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.
J. Biochem. 122, 577-585, 1007
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R;Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced fr
A;Reference number: A33810; MUID:89255254; PMID:2722777
A;Accession: A33810
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C;Species: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A2314; A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                 C: Reywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm F:1-403/Region: cytoskeletal protein binding F:404-911/Region: anion antiporter
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C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
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A; Residues: 1-848 < KUD>
A; Cross-references: GB:J04793; NID:g203092; PIDN:AAA40800.1; PID:g203093
C; Superfamily: band 3 anion transport protein
C; Keywords: alternative splicing; transmembrane protein
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Pred. No. 6.7e-07;
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A:Cross-references: GDB:119874; OMIM:109270
A:Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
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us-10-087-464-2.rpr

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C;Accession: A31789
C;Accession: A31789
R;Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F.
J. Biol. Chem. 263, 17092-17099, 1988
A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney and A;Reference number: A31789; MUID:89034212; PMID:3182834
                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNÅ
A; Residues: 1-1214 <RUUD>
A; Cross-references: GB:J05166; NID:9203090; PIDN:AAA40799.1; PID:9203091
A; Lindsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. SCI. U.S.A. 87, S278-5282, 1990
A; Tille: Functional expression and subcellular localization of an anion exchanger.clo
A; Reference number: A35770; MUID:90319095; PMID:2371270
                                                                                                                                                                                                             two proteins that are rela
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A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual
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A;Residues: 1-205, A'. 207-924,'PG',927-1017,'IV',1020-1155,'ID',1158-1234 <LIN>
C;Superfamily: band 3 anion transport protein
C;Reywords: transmembrane protein
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Am. J. Physiol. 263, 6345-6352, 1992
A;Title: cDNA cloning and localization of a band 3-related protein from ileum.
A;Reference number: A56764; MUID:93035730; PMID:1415547
C.Species: Rattus norvegicus (Norway rat)
C.Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C.Accession: A34911; A35770
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C;Species: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 20-Aug-1999
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C;Accession: A56764
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A;Molecule type: mRNA
A;Residues: 1-1237 <CHO>
A;Residues: 1-1237 <CHO>
A;Cross-references: GB:S45791; NID:g256659; PIDN:AAB23488.1; PID:g256660
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A; Cross-references: GB:404036; NID:9192132; PIDN:AAA65505.1; PID:9309114
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
C; Keywords: transmembrane protein
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                                                                                                                             Rikudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 205, 462-471, 1990
A;Title: cDNA cloning and tissue distribution of mRNAs:
A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.5%; Score 73; DB 2; Le Best Local Similarity 83.3%; Pred. No. 0.00099; Matches 15; Conservative 0; Mismatches 3;
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83.3%; Pred. No. 0.00099;
tive 0; Mismatches 3;
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Matches 15; Conservative
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C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1999
C.Date: 19-Nov-1999
C.Date: 19-Nov-1988 #sequence_revision 19-Nov-1999
C.Date: 19-Nov-1999

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A:Molecule type: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 4-70,'X','709-902 <RES>
A:Cross-references: GB:J02756; NID:9192136; PIDN:AAA37278.1; PID:9553874
B:Demuth, D.R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cloe, L.; Rovera
BMBO J. 5, 1205-1214, 1986
A:Title: Cloning and structural characterization of a human non-erythroid band 3-like pr
A:Reference number: A91039; MUID:86274622; PMID:3015590
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C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A)Cross-references: GB: M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742 R; Kopito, R.R.; Andersson, M.; Lodish, H.F. Biol. Chem. 262, 80375-8040, 1987 A; Biol. Chem. 262, 80375-8040, 1980 A; A; Title: Structure and organization of the murine band 3 gene. A; Reference number: 149524; MUID:87250387; PMID:3036795
                                                                           A; Molecule type: mRNA
A; Residues: 1-929 < KOP>
A; Residues: 1-920 < KOP>
A; Residues: 1-920 < KOP>
A; Cross-references: GB: 30577; NID: 949897; PIDN: CAA26506.1; PID: 949898
B; Kopito, R.R.; Lodish, H.F.
A; Cell. Blochem. 29, 1-17, 1985
A; Title: Structure of the murine anion exchange protein.
A; Reference number: A26086; MuID: 86034211; PMID: 3840489
A; Accession: A26086
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A;Residues: 11-466,'S',468-929 <DEM>
A;Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C;Genetics:
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C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
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    A; Reference number: A25314; MUID:85268011; PMID:2410791
A; Accession: A25314
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band 3 protein, nonerythroid (MEB3) - human (fragment)
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Pred. No. 0.000
0; Mismatches
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Best Local Similarity 83.3%;
Matches 15; Conservative
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band 3-related protein 2 - rat
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Les 19; Conservative
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A; Residues: 1-929 <KO2>
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Matches
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R;Fievet, B.; Gabillat, N.; Borgese, F.; Motais, R.
EMBO J. 14, 5158-5169, 1995
A;Title: Expression of band 3 anion exchanger induces chloride current and taurine tr
A;Reference number: S59861; MUID:96080151; PMID:7489705
A;Accession: S59861
A;Accession: S59861
A;Accession: Score and sequence not shown
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C; Species: Oncorhynchus myxiss (rainbow trout)
C; Date: 07-Apr-1994 #text_change 20-Aug-1999
C; Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 20-Aug-1999
C; Accession: S24318; S36083; S22173
R; Huebner, S.; Michel, F.; Rudloff, V.; Appelhans, H.
Biochem, J. 285, 17-23, 1992
Biochem, J. 285, 17-23, 1992
A; Title: Amino acid sequence of band-3 protein from rainbow trout erythrocytes derive
A; Reference number: S24318; MUID:92344566; PMID:1637296
                                             the
Mol. Cell. Biol. 8, 4416-4424, 1988
A;Title: Two different mRNAs are transcribed from a single genomic locus encoding A;Reference number: A30816; MUID:89039870; PMID:3185555
A;Accession: A30816
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C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 15-Feb_1996 #sequence_revision 01-Mar-1996 #text_change 20-Aug-1999
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A;Residues: 1-304,'G',306-918 <APP>
A;Cross-references: EMBL:X61699; NID:964308; PIDN:CAA43868.1; PID:964309
C;Superfamily: band 3 anion transport protein
C;Keywords: erythrocyte; transmembrane protein
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                                                                                                                                                                                                                                                                                                               Score 71; DB 2; Len
Pred. No. 0.0016;
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Pred. No. 0.033;
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A; Reference number: $22173
A; Accession: $22173
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                                                                                                                                                                                                          A;Cross-references: GB:M23404
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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A; Residues: 71-89;94-114;570-588 <HUE2>
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76.5%;
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66.7%;
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A; Residues: 1-918 <HUE1>
A; Cross-references: EMBL:X61699
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Best Local Similarity 66.7°
Matches 12; Conservative
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-922 <KIM>
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C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C; Accession: 150159
R; Cox, J.V.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
A; Title: Alternative primary structures in the transmembrane domain of the chicken eryth A; Reference number: 150159; MuID:88216609; PMID:2835670
A; Reference number: 150159
A; Accession: 150159
A; Accession: 150159
A; Accession: 150159
A; Residues: 1-844 ccox>
A; Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C; Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cipecies: Homo sapiens (man)
Cipecies: Homo sapiens (man)
Cipate: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
Cipate: 22-Nov-1993 #sequence_revision 130.
Cipate: 22-N
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A30816
A30816
Band 3 amion transport protein (clone pBIIIC1) - chicken
C;Species: Gallus gallus (chicken)
C;Species: 01-Dec-1989 #sequence_revision 30-Sep-1991 #text_change 16-Feb-1997
C;Accession: A30816
R;Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, M.
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A:Experimental source: New Zealand White rabbit, ileal epithelial cells A:Note: sequence extracted from NCBI backbone (NCBIN:115180, NCBIP:115181) C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                              Gaps
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                                                                                                                                           Length 1237;
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                                                                                                                                        Score 73; DB 2; Length 123
Pred. No. 0.00099;
0; Mismatches 3; Indels
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Pred. No. 0.00099;
0; Mismatches 3; Indels
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Pred. No. 0.0014;
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                                                                                                                                                                                                                                                                                                            1057 SVTHANALTVMSKAVAPG 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1060 SVTHANALTVMSKAVAPG 1077
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                                                                                                                                    Query Match 74.5%;
Best Local Similarity 83.3%;
Matches 15; Conservative (
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
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Gaps

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Indels

5

0; Mismatches

Score 61; DB 2; Length 1227; Pred. No. 0.097;

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Rikopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K. Cell 159, 927-937. 189 description of intracellular pH by a neuronal homolog of the erythrocyte anio A; Reference number: A33638; MUID:90075236; PMID:2686841
                               C;Species: Mus musculus (house mouse)
C;Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
                                                                                                                                                                                                                   A; Accession: A33638
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1227 < KOOP>
A; Cross-references: GB:M28383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C; Superfamily: band 3 anion transport protein
     erythrocyte anion exchanger homolog AE3 - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: September 3, 2003, 11:51:18
Job time : 19.25 secs
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Best Local Similarity 72.2%;
Matches 13; Conservative
                                                                                  C; Accession: A33638
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C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: B34911
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
B;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are related A;Reference number: A34911; MUID:90094439; PMID:2294114
                                                                                                                                                                                                                                                                                                                                                                                                          Rilin, S.C.; Kudrycki, K.E.; Shull, G.E.
J. Biol. Chem. 267, 7927-7935, 1992
A;Title: The predicted translation product of a cardiac AE3 mRNA contains an N terminus Apne, and identification of an alternative transcription initiation site.
A;Reference number: A42497; MUID:92218461; PMID:1560021
A;Accession: A42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: this translation is not annotated in Genbank entry RATAE3A, release 111.0; this A;Note: sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A;Accession: B42497
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A,Residues: 1-73, E. <LIN2>
A;Residues: 1-73, E. <LIN2>
A;Cross-references: GB:M87060; NID:g202770; PIDN:AAA40692.1; PID:g202771
A;Experimental source: tissue type spleen
C;Superfamily: band 3 anion transport protein
C;Keywords: alternative splicing; cardiac muscle; heart; transmembrane protein
                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C;Accession: A42497; B42497
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-127 < KUDD.
A; Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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Pred. No. 0.081;
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                            Indels
                                                                                                                                                                                                                                                                            anion exchanger 3, cardiac splice form - rat
N;Alternate names: AE3; chloride/bicarbonate exchanger 3
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Pred. No. 0.097;
Pred. No. 0.033;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: not compared with conceptual translation A;Molecule type: mRNA A;Residues: 1-1030 <LINI>A;Cross-references: GB:M87060; NID:g202770
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                                                                                1 SVTHANALTVMGKASTP 17
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Best Local Similarity 76.5%;
Matches 13; Conservative
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Best Local Similarity 72.2%;
Matches 13; Conservative
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Matches 13; Conservative
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RESULT 15 A33638

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein 3, 2003, 11:41:03 ; Search time 17.25 Seconds September Run on:

(without alignments)
111.500 Million cell updates/sec

US-10-087-464-3 96 1 GKASTPGAAAQIQEVKEQRI 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 seqs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable transport	hypothetical metab	coronin-like prote	non-histone chromo	D-alanyl-D-alanine	hypothetical prote	probable myosin he	probable sodium bi	hypothetical prote	<ul> <li>hypothetical prote</li> </ul>	collagen - nematod	acidic calmodulin-	flagellar biosynth	flagellar biosynth	probable dimethyla	protein F5M15.22 [
н85786	A64937	T38258	T38936	C97305	S60961	A71441	T37460	T22491	C84482	B44984	A46597	AI2647	H97429	H95942	B86338
~	~	~	~	~	~	7	~	7	~	~	~	~	7	~	7
416	452	601	108	241	448	527	1119	1175	159	210	220	251	251	264	265
44.8	44.8	44.8	43.8	43.8	43.8	43.8	43.8	43.8	42.7	42.7	42.7	42.7	42.7	42.7	42.7
43	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1

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Dand 3 anion transport protein, erythrocyte - human N;Alternate names: carrier family 4, anion exchanger, member 1; erythroid anion exchange; Species: Homo sapiens (man) 6;Species: Homo sapiens (man) 7. Species: 0. Species: 0
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-911 <LUX>
A;Cross-references: GB:N27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
B;Cross-references: GB:N27819; NID:g178215; PIDN:AAA35514.1; PID:g178216
B;Tanner, M.J.A.; Martin, P.G.; High, S.
B;Cohem. J. 256, 703-712, 1988
A;Title: The complete amino acid sequence of the human erythrocyte membrane anion-tra
A;Reference number: S03074; MUID:89134172; PMID:3223947
A;Residues: 1-55, E',57-911
A;Residues: 1-55, E',57-911
A;Residues: 1-55, E',57-911
A;Residues: 1.71-75, 1987
A;Cross-references: EMBL:X12609; NID:g28713; PIDN:CAA31128.1; PID:g28714
A;Reference number: 139408; MUID:88031311; PMID:3478298
A;Accession: 139408; MUID:88031311; PMID:3478298
A;Accession: 139408; MUID:88031311; PMID:3478298

A;Molecule type: DNA A;Residues: 37-56 <SHO1> A;Cross-references: GB:M16978; NID:g178217; PIDN:AAA51670.1; PID:g178220 A;Accession: 139409

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C;Comment: Band 3 has at least two functional domains. Its integral domain mediates ing sites for cytoskeletal proteins, glycolytic enzymes, and hemoglobin.
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nes 20; Conserv
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A; Residues: 1-848 <KUD>
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                                                                                                                                                                                                                      A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;435-457/Domain:
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F; 522-542/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;659-680/Domain:
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F;723-743/Domain:
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F;785-806/Domain
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Matches
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A. Molecule type: protein
A. Residues: 834-842, "X, 844-911 < KAW>
A. Molecule type: protein
A. Residues: 834-842, "X, 844-911 < KAW>
A. Molecule type: protein
A. Molecule type: broad to bind the affinity label pyridoxal phosphate, a substrate fc
B. Yannoukakos, D.; Vasseur, C.; Blouquit, Y.; Bursaux, E.; Walcman, H.
Biochim. Biophys. Acta 998, 43-49, 1989
A. Title: Primary structure of the cytoplasmic domain of human erythrocyte protein band 3. A. Accession: 805533
A. Molecule type: protein
A. Residues: 1-201;220-292;307-308, "K',310-312, 'S',314-329, 'K',331-333;347-370 < YANI>
B. A. Residues: 1-201;220-292;307-308, "R',310-312, 'S',314-329, "K',331-333;347-370 < YANI>
B. A. Accession: A3835; MUD: 91070049; PMID: 1701324
A. Accession: A3835; MUD: 91070049; PMID: 1701324
A. Accession: A3835; MUD: 91070049; PMID: 1701324
A. Molecule type: protein
A. Molecule type: Drotein
A. Molecule type: Drot
A:Title: Amino acid sequence of the N(alpha)-terminal 201 residues of human erythrocyte A;Reference number: A92430; MUID:83238395; PMID:6345535
A;Accession: A92430
A;Molecule type: protein
A;Residues: 1-10, 70, 12-68, 76, 76-200 <KAU>
B;Brock, C.J.; Tanner, M.J.A.; Kempf, C.
B;Brock, C.J.; Tanner, M.J.A.; Kempf, C.
B;Accession: A90323; MUID:83308584; PMID:6615451
A;Accession: A90323
A;Molecule type: protein
A;Residues: 559-630 <BRO>
A;Note: Lys-590 was shown to bind phenyl isothiocyanate, an inhibitor of anion transport R; Rawano, Y:; Okubo, K:; Tokumaga, F:; Miyata, T:; Iwanaga, S.; Hamasaki, N.
J. Biol. Chem. 263, 8232-8238, 1988
A;Title: Localization of the pyridoxal phosphate binding site at the COOH-terminal regic
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A; Note: sequence extracted from NCBI backbone (NCBIP:113819, NCBIP:113823, A; Note: a histidine residue essential for anion transport is suggested to be His-651, Hi R; Okubo, K.; Kang, D.; Hamasaki, N.; Jennings, M.L.
Biol. Chem. 269, 1918-1926, 1994
A; Title: Red blood cell band 3. Lysine 539 and lysine 851 react with the same H-2DIDS (4 A; Reference number: A49717; MUID:94124538; PMID:8294441
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A; Molecule type: protein
A; Residues: 361-911 <HAM>
C; Comment: Band 3 is the major integral glycoprotein of the erythrocyte membrane. A dime
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A;Ancleule type: protein
A;Molecule type: protein
A;Note: sequence extracted from NCBI backbone (NCBIP:49829)
A;Note: sequence of a common polymorphic form designated band 3 Memphis
B;Note: sequence of a common polymorphic form designated band 3 Memphis
B;Rang, D.; Okubo, K.; Hamasaki, N.; Shiraki, H.
J. Biol. Chem. 267, 19211-19217, 1992
A;Title: A structural study of the membrane domain of band 3 by tryptic digestion. Confc
A;Reference number: A44116; MUID:92406862; PMID:1527044
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A;Residues: 361-372;390-399;604-613;632-639;647-656;699-729;731-743;761-781;818-826 <KAN
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A; Molecule type: protein

A; Nos. 124-36; 479-519; 538-540; 559-566; 809-817; 825-841; 849-857 < OKU>

A; Nos. 124-539 and Lys-851 were shown to bind the same molecule of the anion transport R; Hamasaki, N.; Okubo, K.; Kuma, H.; Kang, D.; Yae, Y.

Blochem. 122, 577-585, 1997

A; Title: Proteolytic cleavage sites of band 3 protein in alkali-treated membranes: Fidel A; Reference number: PC4403; MUID: 98006310; PMID: 9348087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blood 78, 1117-1120, 1991
A;Title: Human erythrocyte band 3 polymorphism (band 3 Memphis): characterization of
A;Reference number: A44933; MUID:91329825; PMID:1678289
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band 3 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 20-Aug-1999
C;Accession: A25314; A26086; I49524; B25104
R;Kopito, R.R.; Lodish, H.F.
Nature 316, 234-238, 1985
A;Title: Primary structure and transmembrane orientation of the murine anion exchange
                                                                                                C:Keywords: acetylated amino end; glycoprotein; ion transport; phosphoprotein; transm F:1-403/Region: cytoskeletal protein binding F:404-911/Region: anion antiporter
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R;Kudrycki, K.E.; Shull, G.E.
J. Bibl. Chem. 264, 8185-8192, 1989
A;Title: Primary structure of the rat kidney band 3 anion exchange protein deduced A;Reference number: A33810; MUID:89255254; PMID:2722777
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C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                 Domain: transmembrane status predicted <TW04>

Domain: transmembrane status predicted <TW04>

Domain: transmembrane status predicted <TW05>

Domain: transmembrane status predicted <TW05>

Domain: transmembrane status predicted <TW06>

Domain: transmembrane status predicted <TW09>

Domain: transmembrane status predicted <TW09>

Domain: transmembrane status predicted <TW09>

Domain: transmembrane status predicted <TW10>

Domain: transmembrane status predicted <TW12>

Domain: transmembrane status predicted <TW12>

Domain: transmembrane status predicted <TW12>

Appendin: transmembrane status predicted <TW13>

Appendin: transmembrane status predicted <TW13>

Appendin: transmembrane status predicted <TW13>

Appendin: transmembrane status predicted <TW14>

Appendin: transmembrane status experimental status experimental
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F;642/Binding site: carbohydrate (Asn) (covalent) #status pr
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C;Keywords: alternative splicing; transmembrane protein
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95.0%; Pred. No. 1.2e-05;
Live 0; Mismatches 1;
                                                                                                                                                                                                                    predicted
predicted
predicted
                                     A;Map position: 17q21-17q22
C;Superfamily: band 3 anion transport protein
GDB:119874; OMIM:109270
                                                                                                                                                                                                                           transmembrane #status
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les 19; Conservative
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: A30816
C;Accession: A30816
C;Accession: A30816
R;Kim, H.R.C.; Yew, N.S.; Ansorge, W.; Voss, H.; Schwager, C.; Vennstroem, B.; Zenke, Mol. Cell. Biol. 8, 4416-4424, 1988
A)71tile: Two different mRNAs are transcribed from a single genomic locus encoding the A;Reference number: A30816
A;Reference number: A30816
A;Accession: A30816
A;Accession: A30816
A;Residues: 1-922 cKIM>A;Residues: 1-922 cKIM>A;Residues: GB:M23404
C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C; Accession: A25104
R; Demuth, D. R.; Showe, L.C.; Ballantine, M.; Palumbo, A.; Fraser, P.J.; Cioe, L.; Rov EMBO J. 5, 1205-1214, 1986
A; Title: Cloning and structural characterization of a human non-erythroid band 3-like A; Title: Cloning and structural characterization of a human non-erythroid band 3-like A; Reference number: A91039; MUID:86274622; PMID:3015590
A; Accession: A25104
A; Residues: 1-865 <DEN>
A; Residues: 1-865 <DEN>
A; Cross-references: GENX0318; NID:g32120; PIDN:CAA27556.1; PID:g32121
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: A34911; A35770
R;Kudrycki, K.E.; Newman, P.R.; Shull, G.E.
J. Biol. Chem. 265, 462-471, 1990
A;Title: cDNA cloning and tissue distribution of mRNAs for two proteins that are rela A;Reference number: A34911; MUID:90094439; PMID:2294114
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A; Status: preliminary
A; Molecule type: mRM
A; Molecule type: mRM
A; Residues: 1-1234 cKUD>
A; Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
A; Cross-references: GB:J05166; NID:g203090; PIDN:AAA40799.1; PID:g203091
B; Linddsey, A.E.; Schneider, K.; Simmons, D.M.; Baron, R.; Lee, B.S.; Kopito, R.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 5278-5282, 1990
A; Title: Functional expression and subcellular localization of an anion exchanger clo
A; Reference number: A35770; MUID:90319095; PMID:2371270
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band 3 protein, nonerythroid (MEB3) - human (fragment)
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Pred. No. 0.73;
2; Mismatches
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Best Local Similarity 63.2%;
Matches 12; Conservative
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Matches 12; Conservative
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Acst. 150159
R;Cox, JV.; Lazarides, E.
Mol. Cell. Biol. 8, 1327-1335, 1988
Mol. Cell. Biol. 8, 1327-1335, 1988
A;Title: Alternative primary structures in the transmembrane domain of the chicken eryth A;Reference number: 150159; MUID:88216609; PMID:2835670
A;Accession: 150159
A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Superfamily: band 3 anion transport protein
C;Keywords: transmembrane protein
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A;Cross-references: GB:M19496; NID:g211211; PIDN:AAA48604.1; PID:g211212
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Residues: 1-929 <K02>
A)Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
A)Cross-references: GB:M29379; NID:g191741; PIDN:AAA37187.1; PID:g191742
B)Chem. 262, 8035-8040, 1987
A)Title: Structure and organization of the murine band 3 gene.
A)Reference number: 149524; MUID:87250387; PMID:3036795
                                                                                                                                                                                  A; Cross-references: GB: X02677; NID:g49897; PIDN:CAA26506.1; PID:g49898 R; Kopito, R.R.; Lodish, H.F. J. Cell. Biochem. 29, 1-17, 1985 A; Title: Structure of the murine anion exchange protein. A; Reference number: A26086; MUID:86034211; PMID:3840489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 11-466,'S',468-929 <DEM>
A; Cross-references: GB:X03917; NID:953042; PIDN:CAA27555.1; PID:953043
C; Genetics:
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Pred. No. 1.3e-05;
); Mismatches 1; Indels
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A;Reference number: A25314; MUID:85268011; PMID:2410791
A;Accession: A25314
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Pred. No. (
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Best Local Similarity 95.0%;
Matches 19; Conservative (
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Best Local Similarity 60.0°
Matches 12; Conservative
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                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-929 <KOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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ŏ qq A;Accession: A35770
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRMA
A;Molecule type: mRMA
A;Residues: 1-205,'A',207-924,'PG',927-1017,'IV',1020-1155,'ID',1158-1234 <LIN>
C;Superfamily: band 3 anion transport protein

A30816 band 3 anion transport protein (clone pBIIIC1) - chicken

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release 111.0; th
A,Title: Complete nucleotide sequence of band 3 related anion transport protein AE2 A;Reference number: S21086; MUID:92223115; PMID:1562608
A;Accession: S21086
A;Status: preliminary
A;Status: mRNA
A;Molecule type: mRNA
A;Residues: 1-1240 <GEH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 07-Dec-1999
C.Accession: A42497; B42497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rilin, S.C.; Kudrycki, K.E.; Shull, G.E. J. Biol. Chem. 267, 7927-7935, 1992
A; Hile: The predicted translation product of a cardiac AE3 mRNA contains A; Title: The predicted translation product of a cardiac AE3 mRNA contains A; Reference number: A42497; MUID:92218461; PMID:1560021
A; Accession: A42497
                                                                                                                                                                                                                                                                                                                  Gaps
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A; Residues: 1-73, E' <a href="Line">LIN2</a>
A; Experimental source: tissue type spleen
C; Superfamily: Dand 3 anion transport protein
C; Superfamily: Dand 3 anion transport prodein
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A; Residues: 1-1030 <LLIN1>
A; Cross-references: GB:M87060; NID:g202770
A; Orde: Lhis translation is not annotated in GenBank entry RATAE3A, releable sequence extracted from NCBI backbone (NCBIN:96971, NCBIP:96975)
A; Accession: B42497
                                                                                                                                                         PIDN:CAA44067.1; PID:928425
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N/Alternate names: AE3; chloride/bicarbonate exchanger 3
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: alternative splicing; cardiac muscle; heart;
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                                                                                                                                                                                                                                                    DB 7
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Pred. No. 1.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Gehrig, H.; Appelhans, H. submitted to the EMBL Data Library, January 1993 A;Reference number: S31828
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                      A;Cross-references: EMBL:X62137; NID:928424; EC;Superfamily: band 3 anion transport protein C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                               Score 58;
Pred. No.
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Best Local Similarity 63.2%;
Matches 12; Conservative
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C;Date: 06-Jan-1995 #sequence
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Best Local Similarity
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A; Residues: 1-357 <GEH>
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Band 3-related protein - mouse

Band 3-related protein - mouse

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: A31789

C;Accession: A31789

A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney and fr A;Feference number: A31789

A;Title: Cloning and characterization of a murine band 3-related cDNA from kidney and fr A;Feference number: A31789

A;Accession: A31789

A;Molecule type: mRNA

A;Residues: 1-1237 CALP

A;Coss.references: GB:J04036; NID:g192132; PIDN:AAA65505.1; PID:g309114

C;Superfamily: band 3 anion transport protein

C;Reywords: transmembrane protein
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band 3-related protein, ileum - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C; Accession: A56764
R; Chow, A.; Dobbins, J.W.; Aronson, P.S.; Igarashi, P.
Am. J. Physiol. 263, G345-G352, 1992
A; Title: CDNA cloning and localization of a band 3-related protein from ileum.
A; Accession: A56764
A; Accession: A56764
A; Status: preliminary
A; Molecule type: mRNA
A; Status: preliminary
A; Molecule type: mRNA
A; Status: CGDO
A; CTOSS - references: GB: S45791; NID: G256659; PIDN: AAB23488.1; PID: g256660
A; Experimental source: New Zealand White rabbit, ileal epithelial cells
A; Note: sequence extracted from NCBI backbone (NCBIN: 115180, NCBIP: 115181)
C; Superfamily: band 3 anion transport protein
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Aug-1999
C;Accession: S21086
R;Gehrig, H.; Mueller, W.; Appelhans, H.
Biochim. Biophys. Acta 1130, 326-328, 1992
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63.2%; Pred. No. 1;
iive 2; Mismatches
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                                                   Score 58; DB 2
Pred. No. 1;
2; Mismatches
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Pred. No. 1;
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Mismatches
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1069 KAVAPGDKPKIQEVKEQRV 1087
                                                                                                                                                                                   1066 KAVAPGDKPKIQEVKEQRV 1084
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C; Keywords: transmembrane protein
                                                   Query Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
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ilarity 63.2%;
Conservative
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Matches 12; Conserv
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Score 54; DB 2; Length 1232; Pred. No. 4.2; 2; Mismatches 5; Indels

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A; Residues: 1-1232 <RES>
A; Cross-references: EMBL:U05596; NID:g476221; PIDN:AAA50748.1; PID:g476222
C; Superfamily: band 3 anion transport protein
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                                                                                                                                                                                                                                        1066 AIAPGDKPQIQEVREQRV 1083
                                                                                                                                                                                                                       3 ASTPGAAAQIQEVKEQRI
                                                                                                                    Query Match 56.2%;
Best Local Similarity 61.1%;
Matches 11; Conservative
  A; Molecule type: mRNA
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7. Biol. Chem. 265, 462-471, 1980
A;Title: CDNA cloning and tissue distribution of mRNAs for two proteins that are related
A;Reference number: A34911; MUID:90094439; PMID:2294114
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R; Yannoukakos, D.; Stuart-Tilley, A.; Fernandez, H.; Fey, P.; Duyk, G.; Alper, S.
Circ. 55, 603-614, 1994
A; Title: Molecular cloning, expression, and chromosomal localization of two isoforms of A; Reference number: I38496; MUID:95008042; PMID:7923606
A; Accession: I38496
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Kopito, R.R.; Lee, B.S.; Simmons, D.M.; Lindsey, A.E.; Morgans, C.W.; Schneider, K. Cell 59, 927-937, 1989
A;Title: Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion A;Reference number: A33638; MUID:90075236; PMID:2686841
A;Accession: A33638
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 20-Aug-1999
C;Accession: B34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Mus musculus (house mouse)
C;Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 20-Aug-1999
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*Residues: 1-1277 <KOPS
A;Cross-references: GB:MZ8383; NID:g191735; PIDN:AAA37184.1; PID:g309095
C;Superfamily: band 3 anion transport protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-1277 < KUD).
A; Cross-references: GB:J05167; NID:g203088; PIDN:AAA40798.1; PID:g203089
C; Superfamily: band 3 anion transport protein
C; Keywords: transmembrane protein
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Pred. No. 4.2;
2; Mismatches
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  Pred. No. 3.5;
                           Mismatches
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Pred. No. 4
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Best Local Similarity 61.1%;
Matches 11; Conservative ;
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Best Local Similarity 61.18;
Matches 11; Conservative
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Best Local Similarity 61.1%;
Matches 11; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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2: sp_bacteria:*
3: sp_fung1:*
4: sp_human:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_plant:*
sp_rodent:*
sp_rodent:*
sp_vrrus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*

sp_archeap:*

#### SUMMARIES

	Description	091ze7 rattus norv	O9tuq0 bos taurus	09xsw5 bos taurus	090579 gallus gall	035225 cynomys lud	0991t5 mus musculu	09tu75 sus scrofa	08taq3 homo sapien	090710 gallus gall	Oguey4 homo sapien	Q9uey5 homo sapien	099654 homo sapien	Oguey6 homo sapien	099416 homo sapten	013717 homo sapien	O9erp4 mus musculu
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Q9erp5 mus musculu P70877 lamperra ja Q8che2 mus musculu Q35211 mus musculu Q8cb63 mus musculu		015033	Q21664 caenorhabdi Q8msp0 drosophila Q9vp2 drosophila Q9vc29 drosophila Q9x8h5 streptomyce Q8x8h5 streptomyce	095878 Grocerichia 085875 canis famil 0858795 canis famil 0858792 mus musculu 08mrk3 drosophila 08mkf0 bos taurus 08h6x1 arabidopsis 081qd4 drosophila
Q9ERP5 P79877 Q8CHE2 O35211 Q8CB63	Q9RU15 Q9PCQ5 Q986H6 Q9PCQ4 Q8OV71	Q9DQA3 Q910S3 Q9J4L6 Q8QY72 Q8AV16	Q21664 Q8MSP0 Q9VPP2 Q9VCZ9 Q9X8H5 Q8BRD3	QBFGX7 QBFGX7 QBBN92 QBMRX3 QBMKF0 QBHKF0 QBHCX1
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#### ALIGNMENTS

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RESULT 2

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Query Match
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Koshino I., Inaba M., Matsumoto M., Ono K.;
Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
with decreased mutant mRNA possessing dominant negative effect and
dominant hereditary spherocytosis in cattle.";
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF168826; AA043593.1;
HSSP; P02730; 1BNX.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HG03_cotranspt.
Pfam; PF00955; HG03_cotranspt.
                                                                                                                                                                                        TISSUE-Kidney;
Koshino I., Inaba M., Matsumoto M., Ono K.;
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and
                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 70; DB 6; Length 855;
Pred. No. 0.012;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1231; HCO3TRNSPORT.
TIGRRAMS; TIGR00834; ae; 1.
PROSTIE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; P0022020; ANION_EXCHANGER_2; 1.
SEQUENCE 930 AA; 104374 MW; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                                         dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AFI65828; AAD43354.1;
HSSP; PO2730; IBNX.
                                                                                                                                                                                                                                                                                       InterPro; IPR001717; Anion_exchange.
InterPro; IPR0010177; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Promys; PR01231; HCO3-cotranspr.
IGRPAMs; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS0022020; ANION_EXCHANGER_2; 1.
SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
                                    Created)
Last sequence update)
Last annotation update)
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Last sequence update)
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              855 AA.
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              PRT;
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686 KDSTPGAVSQIQGVKEQRI 704
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78.9%;
                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity 78.9
Matches 15; Conservative
              PRELIMINARY;
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                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                   NCBI_TaxID=9913;
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09XSW5
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                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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TISSUB-Gall bladder;
Abbedin Z.R., Moser A.J., Roslyn J.J., Abedin M.Z.;
"Expression of anion exchange protein 2 (AE-2) in gallbladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61; DB 13; Length 844;
Pred. No. 0.35;
3; Mismatches 5; Indels
  Length 930;
                                                   3; Indels
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF012895; AAB66833.1; -.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PR00155; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
TIGRFAMS; TIGR00220; ANION EXCHANGER_1; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TIEMBLTEL. 05, Created)
01-JAN-1998 (TIEMBLTEL. 05, Last sequence update)
01-MAR-2003 (TIEMBLTEL. 23, Last annotation update)
Anion exchange protein 2 (Fragment).
                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
  DB 6;
0.013;
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                                                   1; Mismatches
  Score 70;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cox J.V., Lazarides E.;
"Alternative primary structures in the chicken erythroid anion transporter.";
Mol. Cell. Biol. 8:1327-1335(1988).
EMBL; M19496; ARA48604.1; -.
HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last seq 01-NAR-2003 (TrEMBLrel. 23, Last ann Erythroid anion transporter.
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MEDLINE-88216609; PubMed-2835670;
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| 761 KDSTPGAVSQIQGVKEQRI 779
                                                                                                2 KASTPGAAAQIQEVKEQRI 20
72.9%;
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Best Local Similarity 60.07
Matches 12; Conservative
                                                   Conservative
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                         Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
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Zolotarev A.S., Shmukler B.E., Alper S.L.;
"AEZ anion exchanger polypeptide is a homooligomer in pig gastric membranes: a chemical cross-linking study.";
Blochemistry 38:8521-8531(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
similar to solute carrier family 4, anion exchanger, member (Erythrocyte membrane protein band 3-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 4; Length 1159;
Pred. No. 1.5;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                               Ouery Match 60.4%; Score 58; DB 6; Length 622; Best Local Similarity 63.2%; Pred. No. 0.77; Matches 12; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BCC28601, AAH28601.1; -.
InterPro; IPR001717, Anion_exchange.
InterPro; IPR001717, Anion_exchange.
InterPro; IPR003020, HCO3_cotranspt.
Pfam; PF00955, HCO3_cotranspt. 1.
TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA; 127747 MM; 9F083A2BEBFF5D74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              NON_TER 1 1 SEQUENCE 622 AA; 68713 MW; 58B013462C36E1DC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
AE2-1 anion exchanger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1159 AA.
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                                                                                                                                                                            InterPro; 1PR001717; Anion_exchange.
InterPro; 1PR001717; Anion_exchange.
InterPro; 1PR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
                                     TISSUE-Stomach;
MEDLINE-99315230; PubMed-10387099;
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991 KAVAPGDKPKIQEVKEQRV 1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                              EMBL; AF120099; AAF00977.1;
HSSP; P02730; 1BTQ.
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                    SEQUENCE FROM N.A.
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Q90710;
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Zolotarev A.S., Chernova M.N., Yannoukakos D., Alper S.L.;
"Protoclytic cleavage sites of native AE2 anion exchanger in gastric mucosal membranes.";
Blochemistry 35:10367-10376(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metažoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
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                                                                                      Score 58; DB 11; Length 103;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC002234; AAH02234.1; -
MGD; MG1:109351; S16462.
InterPro; IPR001717; Anion exchange.
InterPro; IPR001717; Anion exchange.
InterPro; IPR00320; HC03_cotranspt.
PR00151; PR01231; HC03_cotranspt.
TIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   466 AA; 52003 MW; 481C1108E28D03B1 CRC64;
                                   103 103
103 AA; 11012 MW; 29A99247E768B455 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment).
                                                                                                                                                                                                                                                                                                          099LT5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
10-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kDa protein (Fragment).
SLC4A2.
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                                                                                                                             2; Mismatches
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Pfam, PF00955; HC03_cotransp; 1. NON_TER 1 1.03 NON_TER 103 SEQUENCE 103 AA; 11012 MW; 2
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67 KAVAPGDKPKIQEVKEQRV 85
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                                                                                        Query Match 60.4%;
Best Local Similarity 63.2%;
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
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SEQUENCE FROM N.A.
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Q9TU75;
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                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                 COX K. H., Adair Kirk T.L., Cox J.V.;
"Variant AE2 anion exchanger transcripts accumulate in multiple cell
types in the chicken gastric epithelium.";
J. Biol. Chem. 271:8895-8902(1996).
EMBL; U48899; AAC59881.1;
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
Pfam; PR00155; HCO3_cotranspt.
Pfam; PR001531; HCO3_cotranspt.
TIGREAMS; TIGR00834; ae; 1.
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Vertebrata; Euteleostomi;
Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";
Blochem. Blophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF19584.2;
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MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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Pred. No. 1.6;
2; Mismatches 5; Indels
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1219 AA; 135288 MW; 25F42A73C3483B21 CRC64;
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1227 AA; 135577 MW; 5D47714C17FB8EF7 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type b1.
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InterPro; IPR003020; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotransp; 1.
PRINTS; PR01231; HGO37FNSPORT.
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EMBL; U76668; AAF19584.2; JOINED.
HSSP; P02730; 1BTQ.
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63.28;
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Best Local Similarity 63.2°
Matches 12; Conservative
AE2.
Gallus gallus (Chicken).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Medina J.F., Lecanda J., Acin A., Ciesielczyk P., Prieto J.;
"Tissue-specific N-terminal isoforms from overlapping alternate prometers of the human AEZ anion exchanger gene.";
Biochem. Biophys. Res. Commun. 267:228-235(2000).
EMBL; U76669; AAF23240.1; -.
EMBL; U76669; AAF23240.1; JOINED.
EMBL; U76669; AAF23240.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=97179202; PubWed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular clonning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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    Length 1227;
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1232 AA; 136218 MW; 22688C662907C2D7 CRC64;
                                                 Indels
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Last annotation update)
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Last annotation update)
    Score 58; DB 4;
Pred. No. 1.6;
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Pred. No. 1.6;
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                                               Mismatches
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PR00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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                                                                                          2 KASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 KASTPGAAAQIQEVKEQRI 20
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63.2%;
60.4%;
ilarity 63.2%;
Conservative
                                                                                                                                                                                                                                                                                               01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23, Anion exchanger 2 type b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIGRFAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                      PRELIMINARY;
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les 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 357;
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Gehriq H., Appelhans H.;
Submitted (JAN-1993) to the EMBL/GenBank/DDBJ databases.
EMBL; X70797; CAA50067.1; -.
InterPro; IPR0012717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; FR003209; HC03_cotranspt.
Pfan; PF00955; HC03_cotranspt 1.
PRINTS; PR01231; HC03TRNSPORT.
PROSTE: PS000220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                               Gehrig H.H., Koenig J., Appelhans H.;
"Alternative anion exchange protein in human kidney.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, X87211; CAA60670.1;
"InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR00320; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357 AA; 39526 MW; 40C03D49F3AF359C CRC64;
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                                                                                                                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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61.1%; Pred. No. 1.9;
cive 2; Mismatches
                                                                                          357 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00955; HC03, cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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                                                                                          PRT;
                                                                                                                                                                                                     Anion exchange protein (Fragment).
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61.1%;
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Matches 11; Conservative
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                                                                                          PRELIMINARY;
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Q99416
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=91179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
EMBL: U65231; AAC50964.1; -.
HSSP; P02730; 1BTQ.
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MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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Pred. No. 1.6;
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Pred. No. 1.6;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 Aa; 137009 MW; D266ECDAB238FD97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                           60.4%; Scor.
63.2%; Pred. No. 1...
2; Mismatches
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Interpro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                          InterPro, IPR001717; Anion_exchange.
InterPro, IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
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Best Local Similarity 63.2,
Loca 12; Conservative
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Search completed: September 3, 2003, 11:50:04 Job time: 45.5 secs

Human erythrocyte
A. tigrinum AE1 pr
Human erythrocyte
Human Band 3 prote

Mouse kidney cell A. tigrinum AE2 pr A. tigrinum AE3 pr Drosophila melanog Haemophilus influe

human secret

Haemophilus influe Haemophilus influe HANBC3 protein sequ NNBC3 protein sequ Human brain-derive Murine Na+-driven Human Na+-driven Human transporter Human transporter Novel human diagno

Human heart muscle Human NT2-2A prote Rickettsia rickett Human Band 3 pepti Human Band 3 pepti Human ORFX protein

Human prostate can Amino acid sequenc A. orientalis gtfB

protein

Human AFP

Human secreted pro Human secreted pro glutamicum prote

Human secreted pro

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
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                                              AAE29344
AAU30825
AAP60645
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WO200270542-A2.
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 AAE29340;
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  Human Band 3 prote
Human Band 3 prote
Human liver peptid
Peptide #6645 enco
Protein #6029 enco
Human brain expres
Human bone marrow
Peptide #6670 enco
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                                                                               3, 2003, 11:24:37; Search time 48.5 Seconds (without alignments) 65.454 Million cell updates/sec
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Score

Result Š 888888888

25450780

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Indels

Score 98; DB 23; Pred. No. 3.7e-09; Mismatches

100.08; 100.0%;

42 AA;

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Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
sequence is human Band 3 protein ectoplasmic domain
                                                                                                                                                                                                                                                                                                                                                                                                Human liver peptide, SEQ ID No 32714.
                                                                                                                                                                                                                                                                                  ABG54066 standard; Peptide; 86 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00664.
                                                                                                                                                                                                                                                                                                                                                            25-FEB-2003 (first entry)
                                                                Ouery Match
Best Local Similarity 100.0
Matches 20, Conservative
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                         ABG54066;
                                       Sequence
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                                                                                                                                                                                                                                                 RESULT 3
ABG54066
 SXC
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                                               The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSPP-1 polypeptide or a polypeptide with any of 8 291.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291-1331 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                             Length 20;
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                                                                                                                                                                                                                                                                                                                                         ; DB 23;
. 1.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Band 3 protein ectoplasmic domain 5.
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 98; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goel V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE29349 standard; peptide; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Page 58; 163pp; English,
                 Claim 1; Page 84; 163pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                   1 SVTHANALTVMGKASTPGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAR-2001; 2001US-272930P
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                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 100...
Local Similarity 100...
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                                                                                                                                                                                                                                                                                                      20 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-SEP-2002.
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                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                          The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human liver single exon encoded peptides of the invention.

Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                        Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 98; DB 22;
1larity 100.0%; Pred. No. 8.4e-09;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                               Claim 27; SEQ ID No 32714; 658pp; English.
WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Chen W, Rank DR,

Hanzel DK,

2000US-0207456. 2000US-0608408. 2000US-0180312

2000US-0632366 2000US-0234687 2000US-0236359 2000GB-0024263 us-10-087-464-2.rag

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Page

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA1305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
            Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human hearts -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; brain expressed exon; gene expression analysis; probe;
microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                        Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; SEQ ID No 25800; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM59792 standard; Protein; 86 AA.
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                                                                                                                                                                                        30-JAN-2001; 2001WO-US00666
                                                                                                                                                                                                                                   2000US-0207456
2000US-0608408
                                                                                                                                                                                                                                                                 2000US-0632366
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2000US-0236359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 20; Conservative
                                                                      congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA;
                                                                                                                               WO200157274-A2.
                                                                                                                                                                                                                                  26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                          21-SEP-2000;
                                                                                                    Homo sapiens
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                                                                                                                                                           09-AUG-2001
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AAM59792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                  foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver
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0
                                                                                                                                                                                                   Peptide #6645 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 86;
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100.0%; Pred. No. 8.4e-09;
iive 0; Mismatches 0;
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                                                                                                              ABB39139 standard; Peptide; 86 AA
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                           SVTHANALIVMGKASIPGAA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
            SVTHANALTVMGKASTPGAA
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les 20; Conserv
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                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                  Human;
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                                                                                   RESULT 4
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for
                                                                                                                                                                                                   present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                 Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #6670 encoded by probe for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 98; DB 22; Length 86; Best Local Similarity 100.0%; Pred. No. 8.4e-09; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                  analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID No 32902; 654pp; English.
                                               DR;
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             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAM32633 standard; Protein; 86
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                                               Chen W,
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2000US-0608408.
2000US-0632366.
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2000GB-0024263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                               Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488897/53
                                                                              WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                    86 AA;
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                       Sequence
                                               Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scierosis, schizophrein, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                   Single exon nucleic acid probes for analyzing gene expression in human brains -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 98; DB 22; 100.0%; Pred. No. 8.4e-09;
                                                                                                                                                                                                                                                                                      Rank DR;
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0236359.
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2000US-0608408
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2000US-0608408
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                                                                                                                                                                                                                                                                                                                  WPI; 2001-483446/52
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             WO200157275-A2
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03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
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30-JUN-2000;
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04-OCT-2000;
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AAM7237 RESULT

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predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                  Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous solerosis; Gaucher's disease; Niemann-Pick disease;
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0
                                                                                                           Length 86;
                                                                                                                                              Indels
                                                                                                         100.0%; Score 98; DB 22;
100.0%; Pred. No. 8.4e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; single exon probe; asthma; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID No 31860; 634pp; English.
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                                                                                                                                                                                                                                                                                                          ABG42195 standard; Peptide; 86 AA
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                                                                                                                                                                                                      45 SVTHANALTVMGKASTPGAA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0632366.
2000US-234687P.
2000US-236359P.
2000GB-0024263.
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2000US-0608408.
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                                                                                                                            Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primary ciliary dyskinesi
hyaline membrane disease.
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                                                                        86 AA;
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21-SEP-2000;
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                              ABG42195;
                                                                          Sequence
                                                                                                           Query Match
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C the eukaryote; and (b) detecting specific phonicisation of detectably labeled nucleic acids from eukaryote lung markh, to a single exon probe, labeled nucleic acids from eukaryote lung markh, to a single exon probe, labeled nucleic acids from eukaryote lung markh, to a single exon probe, labeled nucleic acids from eukaryote lung markh, to a single exon probe, omprising (a) identifying exons from genomic sequence by the method comprising (a) identifying exons from genomic sequence by the method tissues and/or cell types using hybridisation to a single exon accordance by the method accordance and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon accordance by the expression of the exons should be assigned to a single gene; a peptide comprising one of a specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene probes/open reading frames (ORF). The probes are used for gene probes/open reading frames (ORF). The probes are used for gene cuch as asthma, lung cancer, chronic obstructive pulmonary diseases (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary hearmansty-pullak syndrome, sarcoidosis, pulmonary hearmansty-pullak syndrome, sarcoidosis, pulmonary hyeolar proteinosis, Raragener syndrome, sarcoidosis, pulmonary hyeolar proteinosis, Raragener syndrome, sarcoidosis, pulmonary hyeolar proteinosis, Raragener syndrome, sarcoidosis, and hyaline membrane disease. The present sequence is a peptide/protein where the servence data for this total or the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune
the array; identifying exons in a eukaryotic genome, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Senescent cell peptide; ANION 1; COOH; auto immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 8.4e-09;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 98; DB 23;
100.0%; Pred. No. 8.4e-09;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (RESE ) RESEARCH CORP TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR15355 standard; Protein; 911 AA.
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Best Local Similarity 100.
Matches 20; Conservative
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N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
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08-MAR-1992
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The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code for a peptide which is immuno-reactive with antibodies to senescent cell for antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell IgG to senescent cells in vitro or in vivo. The prods. Coan be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as haemolytic anaemia, sickle cell anaemia, and idiopathic as haemolytic anaemia, sickle cell anaemia, and idiopathic such as hematory and arythritis and systemic lupus extyhematosus; and other diseases such as those involved in malaria and cancer. More specifically, the prods, are useful in cosmetic and pharmaceutical companisms, diagnostic kits, and methods for detecting or measuring Abs to SCA, studying cellular againg and extending and treatment configurating anions from a gas or liquid, or diagnosis and treatment configuration and autoimmune mechanisms.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; AEI; anion exchange.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 98; DB 12; Length 911; 100.0%; Pred. No. 1.3e-07; Live 0; Mismatches 0; Indels (
mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW90263 standard; peptide; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     731 SVTHANALTVMGKASTPGAA 750
                                     Disclosure; Fig 1; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SVTHANALTVMGKASTPGAA 20
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Best Local Similarity 100.
Matches 20; Conservative
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منت ت. Davis BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059743/05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYYA ) UNIV YALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, bydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (1) as a target to identify agents that block or stimulate activity of an NBC protein, and identify agents that block or stimulate activity of an NBC protein, and ity as a target to assay for NBC-mediated activity of an NBC protein, and ity as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erythrocyte band 3 anion transporter protein; human; hypercoagulation; iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; EPR; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock mycoardial depression; pancreatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human erythrocyte band 3 anion transporter protein.
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                                       Example 1; Fig 5; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SVTHANALTVMGKASTPGAA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2000; 2000WO-US21101.
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                               911 AA;
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Involves obtaining electron paramagnetic resonance (EPR) or UV spectra of involves obtaining electron paramagnetic resonance (EPR) or UV spectra of intric oxide (NO) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the hemoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasciropic; antiinflammatory; antiarsthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoaquiable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, parients with septic shock who develop myocardial depression, concreatitis and progressive respiratory failure, patients with septic shock who develop myocardial depression, conditions such as architis, asthma, cerebritis, bronchttis and conditions arthritis, asthma, cerebritis, bronchttis and conditions are also used for preserving red blood cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide; malarial infection; drug resistance; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
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physiological effect of a composition comprising hemoglobin which
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 911;
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100.0%; Pred. No. 1.3e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE29343 standard; Protein; 911 AA
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                                                                                                                                                                                                                                                                                                                                which can be used in therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002; 2002WO-US06415
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nes 20; Conservative
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N-PSDB; AAD46978.
                                                                                                                                                                                                                                                                                                                                                                      911 AA;
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a cognate molecule present in the host and subsequently minimising harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection -
                                                                                                                                                                  Gaps
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100.0%; Pred. No. 1.3e-07;
Live 0; Mismatches 0;
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Pred. No. 1.3e-07;
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Best Local Similarity 100.0%;
Matches 20; Conservative 0;
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Matches 20; Conservative
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N-PSDB; AAD46979.
                                                                                                   911 AA;
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells capressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and the proteins are useful in genetic vaccination, to regulate had not on be used to increase stem cell proliferation; to regulate hadmatopolesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAUS510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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                                                                                                                                                                                                                                   AAU30825 standard; Protein; 962 AA
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Tang YT, Liu C, Drmanac RT;
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26-JAN-2001; 2001US-0770160.
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Best Local Similarity 100.0
Matches 20; Conservative
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Human Band 3 prote
Human liver peptid
Peptide #6645 enco
Protein #6029 enco
Human brain expres
Human bone marrow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107863
                     GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAE29349
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Gapop 10.0 , Gapext 0.5
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seq length: 2000000000
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Match Length
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Perfect score:
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Maximum DB s
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Peptide #6670 enco Human peptide enco

ABB39139 ABB24030 AAM59792 AAM72377 AAM32633

Human erythrocyte A. tigrinum AEI pr Human Band 3 prote Human Band 3 prote Novel human secret Mouse kidney cell A. tigrinum AE2 pr Human Bend 3 peptino prosophila melanog Drosophila melanog Human Pregnane X R Human nocleobindin Drosophila melanog S. antiboticus 8, Human nocleobindin Drosophila melanog S. antiboticus 8, Human secreted pro Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia Novel human diagno S. toseosporus dap Drosophila melanog Arabidopsis thalia	drug resistance; vaccine;
AAR15355 AAW90263 AAR46914 AAR29344 AAR29344 AAR29344 AAR29344 AAW90261 AAW90261 AAW90261 AAW90261 AAW90261 AAW90261 AAW90261 AAR57771 AR86494 AAR57777 AAR49667 AAG05687 AAG057774 AAG057774 AAG057774 AAG077775 AAG077774 AAG077775 AAG077775 AAG077775 AAG077775 AAG0777775 AAG0777775 AAG077775 AAG077775 AAG077775 AAG0777775 AAG077775 AAG077775 AAG077775 AAG077775 AAG0777775 AAG07777775 AAG077777777777777777777777777777777777	AA. cial infection; SENT INC. el V; which selective he prevention an
911 12 911 20 911 20 911 20 911 20 911 20 911 20 911 20 911 20 912 20 913 20 914 20 914 92 914 92 915 92 916 92 916 92 916 92 917 92 91	entry) e, B35C. eptide; therapyUSO6415 -272930P H'S MED1 Liu D,
00000000000000000000000000000000000000	1 standard; pe  1; 2003 (first e and 3 peptide, and 3 peptide, piens. 0542-A2. 2002. 2002; 2002WO-U 2001; 2001US-2 ST ELIZABETH' AH, Oh SS, 02-759814/82. llated Band 3 p
0148488789014844978901188489789014849	1 AE29341 AE29341; 7-JAN-20 Iman Ban Iman; Ba FOLOZOBC DIO Sapi DZ OO2705 2-SEP-20 2-MAR-20 SELI-) S AISHI A AISAGE PA TIFACE OP
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42 AA;

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sequence is human Band 3 protein ectoplasmic domain 5.
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   SXC
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                                                                                   The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 peptide.
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                          Claim 1; Page 84; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002; 2002WO-US06415.
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Best Local Similarity 100.
Matches 20; Conservative
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AAE29349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention.
Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly
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                                   Gaps
                                                                                                                                                                                                                                                                                                  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analysing gene expression in human adult liver
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ilarity 100.0%; Pred. No. 1.3e-08;
Conservative 0; Mismatches 0;
 ; Score 96; DB 23;
; Pred. No. 5.6e-09;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                     Human liver peptide, SEQ ID No 32714.
                                                                                                                                                                             ABG54066 standard; Peptide; 86 AA
                                                                                    23 GKASTPGAAAQIQEVKEQRI 42
                                                                  1 GKASTPGAAQIQEVKEORI 20
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    100.0%;
100.0%;
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; 2000US-0608408.
; 2000US-0632366.
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Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
04-OCT-2000;
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA11355-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe encoded protein SEQ ID NO: 31897.
           Protein #6029 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human
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                                         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 96; DB 22; Length 86; 100.0%; Pred. No. 1.3e-08; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                 Chen W, Rank DR;
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20000S-0234687.
20000S-0236359.
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2000US-0608408
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Matches 20; Conservative
                                                                       congenital heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488899/53
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                                                                                                                                WO200157274-A2.
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30-JUN-2000;
03-AUG-2000;
                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                    21-SEP-2000;
27-SEP-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                      Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
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                                                                                                                                                                                                         Peptide #6645 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 31774; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 86;
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100.0%; Pred. No. 1.3e-08;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank DR;
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                                                                                                                ABB39139 standard; Peptide; 86 AA.
                          1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen W,
                                                                                                                                                                                                                                                                                                                                                                                           ; 2000us-0180312.
; 2000us-0207456.
; 2000us-0608408.
; 2000us-0632366.
; 2000us-0236356.
           GKASTPGAAAQIQEVKEQRI
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                                                                                                                                                                         04-FEB-2002 (first entry)
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 AA;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-2000;
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                                                                                                                                              ABB39139;
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ABB24030
                                                                                                   ABB39139
                                                                                    RESULT
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(MOLE-) MOLECULAR DYNAMICS INC.
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04-OCT-2000;
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                                                                                                                                                                                                                                                                                                         AAM32633;
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                                                                                                                                                                                      Query Match
                           Penn SG,
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                                                                                                                                                                                                                                          probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                  The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human bone marrow expressed probe encoded protein SEQ ID NO: 32683.
                                                                                                                                                                                                               Example 4; SEQ ID NO: 31897; 650pp + Sequence Listing; English.
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                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                           04-FEB-2000; 2000US-0180312.
26-MX-2000; 2000US-0207456.
30-UNN-2000; 2000US-068408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234597.
04-OCT-2000; 2000US-0236359.
                                                                                                                                                   Chen W,
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
                                                                                                                                                                                                                                                                                        the probes of the invention.
                                            2001WO-US00667
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2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                    WPI; 2001-483446/52
        WO200157275-A2.
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
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                          09-AUG-2001
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #6670 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                         English.
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                                                                                                                                                                                                      Example 4; SEQ ID NO: 32683; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.3e-08;
Live 0; Mismatches 0;
                                                                                                                                                        analyzing gene expression in human bone marrow
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Chen W, Rank DR;
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2000US-0608408.
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   Hanzel DK,
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                                                       WPI; 2001-488900/53
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les 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic disorder
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with mRNA, and (b) measuring the label detectably bound to each probe of
predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                          Human peptide encoded by genome-derived single exon probe SEQ ID 31860.
                                                                                                                                                                                                                                                                                             Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; Nulmonary haemosiderosis; pulmonary histocytosis; lymphangioleiomyomicosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cillary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spatially-addressable \ set \ of \ single \ exon \ nucleic \ acid \ probes, \ used \ to \ measure \ gene \ expression \ in \ human \ lung \ sampleg \ .
                                                                                              Gaps
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                                                                       Length 86;
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                                                                      100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.3e-08;
ive 0; Mismatches 0;
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                                                                                                                                                                                                    ABG42195 standard; Peptide; 86 AA
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                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0632366.
2000US-234687P.
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                                                                                 Best Local Similarity 100.0
Matches 20; Conservative
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                                               86 AA;
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27-SEP-2000;
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30-JUN-2000;
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                                                 Seguence
                                                                                                                                                                                                                            ABG42195;
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                                                                       Query Match
                                                                                                                                                                             RESULT 9
ABG42195
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the array; Identitying exons in a eutraryoute vomp. Labely

(a) algorithmically predicting at least one exon from genomic sequences

(c) the eukaryote; and (b) detecting specific hybridisation of detectably

(labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,

having a fragment identical to the predicted exon, the probe is included

(c) in the above mentioned microarray; assigning exons to a single gene,

(c) comprising (a) identifying exons from genomic sequence by the method

(c) microarrays having a probe with the exon, where a common pattern of

(c) microarrays having a probe with the exon, where a common pattern of

(c) microarrays having a probe with the exon, where a common pattern of

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a peptide comprising one

(c) the exons should be assigned to a single gene, a gene, particularly

(c) the exons should be assigned to a single gene, a gene, particularly

(c) the exons should be assigned to a single gene, a gene, particularly

(c) the exons should defense, (o) the probasis, gaucher, gaisease

(c) the exons should desase, Hermansky-Pudlas syndrome, sarcoidosis, pulmonary

(c) the meann-pick disease, Hermansky-Pudlas syndrome, fibrocystic

(c) the meann-pick disease, Hermansky-Pudlas syndrome, fibrocystic

(c) pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic

(c) pulmonary alveolar proteinosis, Karagener syndrome, ga peptide/protein

(c) encoded by a single exon probe of the invention.

(c) the exons prode of the invention.

(c) the exons the exon probe of the invention.
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the array; identifying exons in a eukaryotic genome, comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human erythrocyte membrane anion-transport protein (band 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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Matches 20; Conservative
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N-PSDB; AAQ15172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1991;
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08-MAR-1992
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The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 588-554 (ANION 1) or 812-827 (COCH) code for a peptide which is immuno-reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cells in vitro or in vivo. The prodes can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as homocytopenia purpura; other autoimmune disease mechanisms, such as rheumatoid arthritis and systemic lupus erythematosus; and other diseases such as those involved in malaria and cancer. More specifically, the prodes are useful in cosmetic and pharmaceutical compsns., diagnostic kits, and methods for detecting or measuring has constant diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NBC; sodium bicarbonate transporter family; pH regulation; immunoassay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; ABI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating
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Is BA, Grichtchenko II, Romero MF, Schmitt BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 911;
 mechanisms, separate anions and treat auto-immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 96; DB 12; 100.0%; Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW90263 standard; peptide; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 74pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. tigrinum AE1 protein.
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Choi I, Davis BA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ambystoma tigrinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                          911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYYA') UNIV YALE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                 This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (1) as a target to identify agents that block or stimulate activity of an NBC protein, and identify agents that block or stimulate activity of an NBC protein, and it was a target to assay for NBC-medatated activity of an NBC protein, and it was a target to assay for NBC-medatated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iron-nitrosyl hemoglobin, electron paramagnetic resonance; UV spectra;
EPR; nitric oxide; antianemic; antibacterial; immunosuppressive;
vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the predominant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Erythrocyte band 3 anion transporter protein; human; hypercoagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock myocaddial depression; pencreatitis; sickle cell crisis; urinary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 Length 911;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 96; DB 20;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                   Example 1; Fig 5; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 20; Conservative
disorders mediated by NBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-183002/18.
                                                                                                                                                                                                                                                                                                                                                           911 AA;
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involves obtaining electron paramagnetic resonance (EPR) or UV spectra of introducing the moglobin derivatives formed by incubation of limiting nitron-nitrosyl hemoglobin derivatives formed by incubation of limiting nitron-nitrosyl hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the hemoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antihilammatory; antiasthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoaquiable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression, pancreatitis and progressive respiratory failure, patients with septic shock who develop myocardial depression, concretitis and progressive respiratory failure, patients with sischemia, patients in a sickle cell crisis and for treating inflammatory conditions such as arthritis, asthma, cerebritis, bronchitis and vasculations are also used for preserving red blood cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide; malarial infection; drug resistance; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
physiological effect of a composition comprising hemoglobin which
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 911;
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                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 96; DB 22;
100.0%; Pred. No. 1.8e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                       which can be used in therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Band 3 protein #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002-759814/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD46978.
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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             harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present sequence is human Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                 Gaps
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cognate molecule present in the host and subsequently minimising
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                                                                                                                                 Length 911;
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                                                                                                                                                                 Indels
                                                                                                                              Score 96; DB 23;
Pred. No. 1.8e-07;
Mismatches 0;
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100.0%; Pred. No. 1.8e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 107-110; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goel V;
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                                                                                                                                                                                                                   742 GKASTPGAAAQIQEVKEQRI 761
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                                                                                                                                                                                                                                                                                                                  AAE29344 standard; Protein; 911
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                                                                                                                                                                                                 1 GKASTPGAAQIQEVKEQRI
                                                                                                                              Match 100.0%;
Local Similarity 100.0%;
tes 20; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002; 2002WO-US06415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2001; 2001US-272930P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Human Band 3 protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-759814/82.
N-PSDB; AAD46979.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911 AA;
                                                                                                911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200270542-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chishti AH,
                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                   AAE29344;
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                                                                                                  Sequence
                                                                                                                                Query Match
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                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                    AAE2934
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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abstrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically encoding them are also useful for producing the proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopolesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone, cartilage, tendon and/or nerve tissue growth or regeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                                                         AAU30825 standard; Protein; 962 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #1316
742 GKASTPGAAAQIQEVKEQRI 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-2001; 2001WO-US08656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-611725/70.
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                                                                                                                                                                                                                                                                                                                        AAU30825;
                                                                                                                                             RESULT 15
AAU 30825
ID AAU 30825
ID AAU 30
XX
AC AAU 30
XX
DT 18-DF
XX
DE NOVE.
XX
DE NOVE
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ö Indels ô Query Match
100.0%; Score 96; DB 22;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 20; Conservative 0; Mismatches 0; õ

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Search completed: September 3, 2003, 11:46:12 Job time : 49.5 secs

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us-10-087-464-4.rag

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September 3, 2003, 11:24:37; Search time 48.5 Seconds (without alignments) 65.454 Million cell updates/sec
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:
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/SIDS1/gcgdata/geneseq/genesegp-emb1/AA1999.
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
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Listing first 45 summaries
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1 DRILLLFKPPKYHPDVPYVK 20
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human Band 3 pepti	Human Band 3 prote	Exofacial region 1	Human band 3 prote	Human erythrocyte	A. tigrinum AEl pr	Human erythrocyte	Human Band 3 prote	Human Band 3 prote
CHTANAMO				342	350	095	988	355	263	914	343	344
200			QI .	AAE29	AAE29350	AAW01	AAB74	AAR15	AAW90	AAB46	AAE29	AAE29
			BB	23	23	17	22	12	20	22	23	23
			Match Length DB	20	51	28	58	911	911	911	911	911
	æ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	112	112	112	112	112	112	112	112	112
		Result	No.		7	m	4	S	9	7	89	6

New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial infection

A HAAAAAA GGG HGG GXGG AA	Human bone marrow Human polypeptide Human suppressor o Novel human protei Human suppressor o Aged band 3 peptid Human adipose tiss
AAU30825 AAW18594 AAW18595 AAW01080 AAW00262 AAW90261 AAW90261 AAW90261 AAW90260 AAW90260 AAW90260 AAW90260 AAW90260 AAW90260 AAW90260 AAW90260 AAW90260 AAW90280 AAW90280 AAW90280 AAW90080 AAW90080 AAW90080 AAW93334 AAW93334 AAW93334 AAW93334 AAW93334	AAM00759 ABB79586 ABB79586 ABP60995 ABP555448 AAW18606 AAM48755
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962 114 117 10340 10340 1035 1035 1037 1037 1038 1038 1038 1038	348 440 440 440 310
0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000	51.8 51.8 51.8 51.8 469.1
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## ALIGNMENTS

Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine; protozoacide; gene therapy. (SELI-) ST ELIZABETH'S MEDICAL CENT INC Chishti AH, Oh SS, Liu D, Goel V; AAE29342 standard; peptide; 20 AA. 01-MAR-2002; 2002WO-US06415. 02-MAR-2001; 2001US-272930P. Human Band 3 peptide, B36A. (first entry) WPI; 2002-759814/82. WO200270542-A2. Homo sapiens. 12-SEP-2002. 27-JAN-2003 AAE29342; RESULT 1 

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The invention relates to an isolated Band 3 polypeptide that comprises any of 4 20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8 291.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and a cognate molecule present in the host and subsequently minimising therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria, The present sequence is human Band 3 peptide.
                               Page 84; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;
                                                                             Human Band 3 protein ectoplasmic domain 6.
                                                   AAE29350 standard; peptide; 51 AA.
                     Query Match
Best Local Similarity 100...
                                                                                          protozoacide; gene therapy
                                                                     (first entry)
                                                                     27-JAN-2003
                                                            AAE29350;
                                           RESULT
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Gaps

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Length 20; Indels

Score 112; DB 23; Pred. No. 6.6e-10; Mismatches

100.0%; 100.0%;

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01-MAR-2002; 2002WO-US06415. WO200270542-A2. Homo sapiens 12-SEP-2002.

Goel V; Liu D, Chishti AH, Oh SS,

(SELI-) ST ELIZABETH'S MEDICAL CENT INC.

02-MAR-2001; 2001US-272930P

WPI; 2002-759814/82

New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial Example; Page 58; 163pp; English. infection

The invention relates to an isolated Band 3 polypeptide that comprises any of 4.20 residue amino acid sequences, or their fragments that bind to an MSP-1 polypeptide or a polypeptide with any of 8.31.131 base pair sequences. The methods and compositions of the present invention are useful for the prevention and treatment of malarial infection. The present invention, develops new and more improved methods based upon inhibiting the particular interactions between the malarial parasite and harmful side effects and drug resistance that may be due to non-specific therapeutic approaches. The invention is useful in gene therapy. The present invention also provides a vaccine for malaria. The present

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Gaps

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Indels

Length 58;

100.0%; Score 112; DB 17; ilarity 100.0%; Pred. No. 2.1e-09; Conservative 0; Mismatches 0;

Local Similarity nes 20; Conserv

Query Match Best Loc Matches

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AAW01053-W01095 represent peptides isolated from (or based on) regions of the anion transporter band 3 protein. The band 3 protein is present in a million copies per red blood cell, in the form of monomers, dimers, or tetramers. Band 3 protein has two distinct domains, a 43 kD water solubbe cytoplasmic domain, and a 55 kD membrane spanning domain. In an number of otherwise-unrelated conditions (such as malaria, and diabetes), there are modifications in band 3, such that there is clustering and a change in the conformation of the protein. Due to this change in protein conformation (and by the exposure of cryptic adhesive sites), the normally non-adherent erythrocyte becomes a cell with enhanced endothelial adhesiveness. These sequences compete with the altered band 3 protein, and thereby block the adhesiveness of the red blood cells. The peptides can be used for reducing the adhesiveness of red blood cells in a mammalian patient characterised by a condition selected from plasmodium falciparum
                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                               Anion transporter band 3 protein; endothelial adhesion; red blood cell; cytoplasmic domain; errythrocyte; exofacial loop; epitope; antibody; mammal; plasmodium falciparum infection; sickle cell disease; diabetes; band 3; thalassaemia; anaemia; therapy.
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide(s) with amino acid motifs in band 3 - used for reducing the adhesiveness of red blood cells for treating malaria, sickle cell
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                                                                                                                                                                                                                                                                                                                                                                               Exofacial region loop 7 of band 3 protein (residues 800-857).
                                                                       Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection, sickle cell disease, thalassaemia and diabetes
                                                                                                         Indels
sequence is human Band 3 protein ectoplasmic domain 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shohet SB, Thevenin BJ;
                                                                 Score 112; DB 23;
Pred. No. 1.8e-09;
Mismatches 0;
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                                                                                                                                           1 DRILLLFKPPKYHPDVPYVK 20
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                                                                                                                                                                                                                                                                     AAW01095 standard; peptide; 58
                                                                   100.0%;
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                                                                   Query Match 100.0
Best Local Similarity 100.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-442944/44.
                                   51 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9629086-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                           08-MAY-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                                                                                                                                                                   RESULT 3
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Wed Sep

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Human erythrocyte membrane anion-transport protein (band 3).
                                                                                                                                                                                                                 Senescent cell peptide; ANION 1; COOH; auto immune disease.
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                                        AAR15355 standard; Protein; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-369184/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ15172.
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                            24-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1990;
                                                                                                                    25-MAR-2003
08-MAR-1992
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                                                                                                                                                                                                                                                                                                                                        28-NOV-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay MBM,
                                                                                 AAR15355;
    RESULT 5
AAR15355
                                                                                                   The present invention describes a method for enhancing thrombolysis in a mammal. The method comprises the administration to the mammal an amount of an inhibitor (I) of protein band 3-ligand interaction

Sufficient to enhance thrombolysis. (I) has thrombolytic activity.

The method is useful for enhancing thrombolysis in a mammal. (I) is useful for enhancing fibrinolytic or thrombolytic activity, in the management of acute myocardial infarction, for lysis of intracoronary thrombl, for improvement of ventricular function, for reduction of congestive heart failure, for reduction of mortality, for the lysis of pulmonary emboli blocking blood flow to one or more lobes of the lung, for the lysis of acute arterial thrombosis and embolism, for the lysis of thrombosis in deep veins or in cerebral sinuses, to reopen i.v. catheers obstructed by clotted blood or fibrin, to prevent clot formation of lysing clots, to prevent clotting in blood samples drawn from patients for clinical testing and to prevent the recurrence of thrombosis in patients by prophylactic administration. The present sequence represents a human band 3 protein predicted exofacial region invention.
                                                                                                                                                                                                                                                                                             Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein; thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction; lysis; ventricular function; congestive heart failure; mortality; acute arterial thrombosis; embolism; thrombosis; cerebral sinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enhancing thrombolysis in mammals comprises administering an inhibitor of protein band 3-ligand interaction
                                                                                                                                                                                                                                                        Human band 3 protein predicted exofacial region loop 7 SEQ ID NO:43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 112; DB 22;
1 Similarity 100.0%; Pred. No. 2.1e-09;
20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Von Andrian U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 7; 23pp; English
                                                                                                                                      AAB74886 standard; peptide; 58 AA.
                    DRILLEKPPKYHPDVPYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0985499.
                                                                                                                                                                                                               19-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA. (BLOO-) CENT BLOOD RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shohet SB, Sherman I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-307101/32.
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0-FEB-2001
                                                                                                                                                                             AAB74886;
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                                                                                                                    AAB74886
                                                                                                   RESULT
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91WO-US03557.

Marchalonis JJ;

(first entry)

(updated)

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The amino acid sequence is that of the human erythrocyte anion-transport protein (band 3). Amino acids 538-554 (ANION 1) or 812-827 (COOH) code for a peptide which is immuno-reactive with antibodies to senescent cell antigen (SCA). The antigen and peptides can be used in any method or technique involving or requiring the inhibition of the binding of senescent cell IgG to senescent cells in vitro or in vivo. The prods can be used in to examine various physiological, biochemical, and immunological mechanisms in humans and other animals, such as those relating to cellular ageing, degeneration, and life span; removal of senescent cells; anion transport across cellular membranes; disease mechanisms where increased senescent cell IgG may play a role, such as haemolytic anaemia, sickle cell anaemia, and idiopathic thrombocytopenia purpura; other autoimmune disease mechanisms, such as haemolytic anaemia sickle cell anaemia, and idiopathic thrombocytopenia purpura; other autoimmune disease mechanisms, and other diseases such as those involved in malaria and cancer. More specifically, the prods are useful in cosmetic and pharmaceutical companisms, diagnostic kits, and methods for detecting or measuring contactions and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abs to SCA, studying cellular ageing and autoimmune mechanisms, separating anions from a gas or liquid, or diagnosis and treatment of certain diseases (Updated on 25-MAR-2003 to correct PA field.)
Synthetic senescent cell antigen and peptide(s) - used to detect antibodies to SCA, study cellular ageing and auto-immune mechanisms, separate anions and treat auto-immune disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW90263 standard; peptide; 911 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  807 DRILLLEKPPKYHPDVPYVK 826
                                                                                                                                                                         Disclosure; Fig 1; 74pp; English.
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AAW90263
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Gaps

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Indels

1 DRILLLFKPPKYHPDVPYVK 20 

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This sequence represents the anion exchange protein AEI which is used in a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate activity of an NBC, (iii) in methods to identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays for detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                     NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; cell proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; ABI; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating disorders mediated by NBC
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                                                                                                                                                                                                                                                                                                                                                                                                                    Aalkjaer C, Bevensee MO, Biemesderfer D, Boron WF;
Choi I, Davis BA, Grichtchenko II, Romero MF, Schmitt BM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 112; DB 20; Length 911;
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Mismatches 0;
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Best Local Similarity 100.0%;
Matches 20; Conservative 0
                                                                                                                                                                                                                                                                                                                98WO-US10297.
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                                                  27-APR-1999 (first entry)
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                                                                                  A. tigrinum AE1 protein.
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                                                                                                                                                                                                             Ambystoma tigrinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        911 AA;
                                                                                                                                                                                                                                                                                                                                                                                     (UYYA ) UNIV YALE.
                                                                                                                                                                                                                                            WO9853067-A1
                                                                                                                                                                                                                                                                                                                20-MAY-1998;
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                                                                                                                                                                                                                                                                              26-NOV-1998
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AAB46914
XEXEXEX
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physiological effect of a composition comprising hemoglobin which involves obtaining electron paramagnetic resonance (EPR) or UV spectra of iron-nitrosyl hemoglobin derivatives formed by incubation of limiting nitric oxide (NO) with hemoglobin and determining if the composition shows non-cooperativity or cooperativity in binding of NO to the memoglobin. The products of the invention have antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic and cerebroprotective activity. The products of the invention are used to produce methods of therapy for medical disorders characterized by red blood cell membrane defects and for a variety of hypercoagulable and vasculopathic states, particularly for patients with septic shock who develop myocardial depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pancreatitis and progressive respiratory failure, patients with septicemia as a complication of urinary tract infection and patients with stochmia, patients in a sickle cell crisis and for treating inflammatory conditions such as arthritis, asthma, cerebritis, bronchitis and vasculitis. The methods are also used for preserving red blood cells
Erythrocyte band 3 anion transporter protein; human, hypercoagulation; iron-nitrosyl hemoglobin; electron paramagnetic resonance; UV spectra; EPR; nitric oxide; antianemic; antibacterial; immunosuppressive; vasotropic; antiinflammatory; antiasthmatic; respiratory; antiarthritic; cerebroprotective; red blood cell membrane defect; vasculopathy; septic shock mycoardial depression, pancreatthis; sickle cell crisis; urhary tract infection; progressive respiratory failure; septicemia; ischemia; arthritis; asthma; cerebritis; bronchitis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel method for determining the predominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining predominant physiological effect of composition comprising hemoglobin used to produce methods of therapy for medical disorders by using EPR or UV spectra of iron nitrosyl hemoglobin derivatives
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100.0%; Pred. No. 4e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE29343 standard; Protein; 911 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 11; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Singel DJ;
                                                                                                                                                                                                                                                                                                                                 02-AUG-2000; 2000WO-US21101.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (RERE-) RES & DEV INST INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOW AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-183002/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      (UYDU-) UNIV DUKE.
                                                                                                                                                                                                                                            WO200109616-A2.
                                                                                                                                                                                                                                                                                                                                                                         02-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stamler JS,
                                                                                                                                                                                                                                                                                      38-FEB-2001
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(SELI-) ST ELIZABETH'S MEDICAL CENT INC.

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Human; Band 3 polypeptide; malarial infection; drug resistance; vaccine;
protozoacide; gene therapy.
                                                                                                                                                                                                                                                                                                      New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
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                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 102-105; 163pp; English.
                                                                                                                                                                                                (SELI-) ST ELIZABETH'S MEDICAL CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE29344 standard; Protein; 911 AA
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                                                                                                                                                                  02-MAR-2001; 2001US-272930P.
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                                                                                                                                    01-MAR-2002; 2002WO-US06415
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Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                         WPI; 2002-759814/82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 911 AA;
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                                                                          WO200270542-A2.
                                             Homo sapiens
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                                                                                                        12-SEP-2002
                                                                                                                                                                                                                                                                                                                                       infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                             New isolated Band 3 polypeptide which selectively binds to merozite surface protein-1, useful for the prevention and treatment of malarial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 112; DB 23;
100.0%; Pred. No. 4e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                Disclosure; Page 107-110; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human secreted protein #1316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 20; Page 354; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU30825 standard; Protein; 962 AA.
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26-JAN-2001; 2001US-0770160.
                                     Liu D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20; Conservative
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                                                                               WPI; 2002-759814/82.
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Best Local Similarity
Matches 20; Conserv
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                                                                                                   N-PSDB; AAD46979
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AAU30825
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polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are useful for identifying agents (agonists and antaponists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides we cells genetically the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU2510-AAU3304 represent the amino acid sequences of novel human secreted proteins of the invention. invention relates to novel human secreted polypeptides. The 962 AA; Sequence 

Length 962; Indels 100.0%; Score 112; DB 22; 100.0%; Pred. No. 4.2e-08; 0; Mismatches 1 DRILLLFKPPKYHPDVPXVK 20 Best_Local Similarity 100. Matches '20; Conservative Query Match 셤 ŏ

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Gaps

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AAW18594

AAW18594 standard; peptide; 16 AA

AAW18594;

(first entry) 04-MAR-1998 Aged band 3 peptide (residues 812-827) epitope I.

Band 3 protein; antibody; aging antigenic site; Alzheimer's disease; phosphorylation; detection; epitope. 

Homo sapiens

WO9726537-A1

24-JUL-1997.

96WO-US20465 13-DEC-1996; (RESE ) RESEARCH CORP TECHNOLOGIES INC.

96US-0010250

19-JAN-1996;

WPI; 1997-385478/35.

Detecting Alzheimer's disease using antibody that recognises aged band 3 protein in tissues - or from reduced degree of band 3 protein phosphorylation, can be applied to blood or brain samples

Claim 6; Page 11; 45pp; English.

This is an aging antigenic band 3 peptide (residues 812-827) to which a specific antibody can bind to. Band 3 is a ubiquitous anion-exchange protein and ages as cells and tissues age. Antibodies have been developed against this aged band 3. These antibodies bind to distinct regions of band 3 in old cells (aging antigenic sites) but not middle aged or young cells. This can be used for detecting Alzheimer's disease. A tissue sample containing band 3 from a patient suspected of having Alzheimer's disease is treated with an antibody that can differentiate between the Alzheimer's (aged) and normal band 3, under complex-forming conditions

in the suspect sample indicates Alzheimer's disease.

This is an aging antigenic band 3 peptide (residues 812-830) to which a specific antibody can bind to. Band 3 is a ubiquitous anion-exchange protein and ages as cells and tissues age. Antibodies have been developed can stain this aged band 3. These antibodies bind to distinct regions of band 3 in old cells (aging antigenic sites) but not middle aged or young cells. This can be used for detecting Alzheimer's disease. A tissue sample containing band 3 from a patient suspected of having Alzheimer's disease is treated with an antibody that can differentiate between the Alzheimer's (aged) and normal band 3, under complex-forming conditions and detecting any complex formed. A tissue containing band 3 from a healthy control is treated in a similar manner and the amounts of complex formed are compared. A significantly greater formation of complex in the suspect sample as compared with that of the control is indicative of Alzheimer's disease. The disease can also be detected by comparing the degrees of phosphorylation of band 3 or its degradation products in suspect and control samples. A significant decrease in phosphorylation ö and detecting any complex formed. A tissue containing band 3 from a healthy control is treated in a similar manner and the amounts of complex formed are compared. A significantly greater formation of complex in the suspect sample as compared with that of the control is indicative of Alzheimer's disease. The disease can also be detected by comparing the degrees of phosphorylation of band 3 or its degradation products in suspect and control samples. A significant decrease in phosphorylation in the suspect sample indicates Alzheimer's disease. Detecting Alzheimer's disease using antibody that recognises aged band 3 protein in tissues – or from reduced degree of band 3 protein phosphorylation, can be applied to blood or brain samples Band 3 protein; antibody; aging antigenic site; Alzheimer's disease; phosphorylation; detection; epitope. ö Length 16; Indels Aged band 3 peptide (residues 812-830) epitope II. DB 18; L 100.0%; Pred. No. 1.4 ive 0; Mismatches 79.5%; Score 89; (RESE ) RESEARCH CORP TECHNOLOGIES INC. AAW18595 standard; peptide; 19 AA. Claim 7; Page 10; 45pp; English. 96WO-US20465. 96us-0010250 6 LEKPPKYHPDVPYVK 20 1 LFKPPKYHPDVPYVK 15 04-MAR-1998 (first entry) Best Local Similarity 100. Matches 15; Conservative WPI; 1997-385478/35. 16 AA; 13-DEC-1996; Homo sapiens WO9726537-A1 19-JAN-1996; Sequence AAW18595; Query Match RESULT 12 AAW18595 888888888888 à 셤

1 KPPKYHPDVPYVK 13

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AAB74852 standard; peptide; 14 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW01053-W01095 represent peptides isolated from (or based on) regions of the anion transporter band 3 protein. The band 3 protein is present in a million copies per red blood cell, in the form of monomers, dimers, or tetramers. Band 3 protein has two distinct domains, a 43 kD or tetramers. Band 3 protein has two distinct domains, a 43 kD or tetramers. Dimersise the and a 55 kD membrane spanning domain. In an number of otherwise-unrelated conditions (such as malaria, and diabetes), there are modifications in band 3, such that there is clustering and a change in the conformation of the protein. Due to this change in protein conformation (and by the exposure of cryptic adhesive sites), the normally non-adherent erythrocyte becomes a cell with cannaced endothelial adhesiveness. These sequences were found in the putative exofacial loops of band 3, and are epitopes for antibody binding. These sequences compete with the altered band 3 protein, and thereby block the adhesiveness of the red blood cells. The peptides can be used for reducing the adhesiveness of red blood cells in a mammallan patient characterised by a condition selected from plasmodium falciparum infection, sickle cell disease, thalassaemia and diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                     Anion transporter band 3 protein; endothelial adhesion; red blood cell;
                                                                                                                                                                                                                                                                                                                                                                                                                     cytoplasmic domain; erythrocyte; exofacial loop; epitope; antibody; mammal; plasmodium falciparum infection; sickle cell disease; diabetes; band 3; thalassaemia; anaemia; therapy.
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide(s) with amino acid motifs in band 3 - used for reducing the adhesiveness of red blood cells for treating malaria, sickle cell
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                               Score 89; DB 18; Length 19;
Pred. No. 1.7e-06;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thevenin BJ;
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                                                                                                                                                                                                                                              AAW01080 standard; peptide; 14 AA.
                   79.5%; Scu.
100.0%; Pre
0;
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                                                                                                                                 1 LEKPPKYHPDVPYVK 15
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                                                                         15; Conservative
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                                 Query Match
Best Local Similarity
19 AA;
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 Sequence
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                                                                         Matches
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                                                                                                                                                                                                            RESULT
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a mammal. The method comprises the administration to the mammal an amammal. The method comprises the administration to the mammal and amount of an inhibitor (1) of protein band 3-ligand interaction amount of an inhibitor (1) of protein band 3-ligand interaction.

Sufficient to enhance thrombolysis. (1) has thrombolytic activity.

The method is useful for enhancing thrombolysis in a mammal. (1) is useful for enhancing fibrinolytic or thrombolytic activity, in the management of acute myocardial infarction, for lysis of intracoronary thrombi, for improvement of ventricular function, for reduction of congestive heart failure, for reduction of mortality, for the lysis of pulmonary emboli blocking blood flow to one or more lobes of the lung, for the lysis of acute arterial thrombosis and embolism, for the lysis of thrombosis in deep veins or in cerebral sinuses, to reopen i.v. catheters obstructed by clotted blood or fibrin, to prevent clot formathon of lysing clots, to prevent clotting in blood samples drawn from patients for clinical testing and to prevent the recurrence of thrombosis in patients band 3 protein loop 3 related peptide, which is sigiven in the exemplification of the present invention.
                                                                                                                                                                                                        Anti-Plasmodium falciparum; interaction inhibitor; band 3 protein; thrombolysis; thrombolytic; fibrinolytic; acute myocardial infarction; lysis; ventricular function; congestive heart failure; mortality; acute arterial thrombosis; embolism; thrombosis; cerebral sinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enhancing thrombolysis in mammals comprises administering an inhibitor of protein band 3-ligand interaction
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                                                                                                                                          Band 3 protein loop 3 related peptide SEQ ID NO:9.
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3.7e-05;
thes 0;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shohet SB, Sherman I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-307101/32.
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                                                                     19-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
AAB74852;
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Gaps

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0; Indels

70.5%; Score 79; DB 17; Length 14; 100.0%; Pred. No. 3.7e-05;

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13; Conservative

Query Match Best Local Similarity Matches 13; Conserva

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a method resulting in the isolation of a novel salamander sodium bicarbonate transporter (NBC). NBC proteins and nucleic acid sequences may be used to treat pathological processes including water retention, increased blood pressure, chronic respiratory and metabolic acidosis, inflammation, cell proliferation, cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma and colitis. Members of the NBC family of proteins can be used (i) as a target to identify agents that block or stimulate NBC mediated pH regulation, (ii) as a target or bait to identify and isolate binding partners that bind NBC, (iii) in methods to identify agents that block or stimulate activity of an NBC protein, and (iv) as a target to assay for NBC-mediated activity. Anti-NBC antibodies are also useful as modulators of NBC activity, useful in the immunoassays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the anion exchange protein AE2 which is used in
                                                                                                                                                 NBC; sodium bicarbonate transporter family; pH regulation; immunoassay; treatment; water retention; blood pressure; acidosis; inflammation; call proliferation; cancer; sperm activation; inactivation; epilepsy; hydroencephaly; glaucoma; colitis; salamander; AE2; anion exchange.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detecting NBC expression/activity and for purifying an NBC protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding proteins of the Sodium Bicarbonate Cotransporter (NBC) family - useful for identifying agents that agonise or antagonise NBC activity and treating disorders mediated by NBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Bevensee MO, Biemesderfer D, Boron WF;
Davis BA, Grichtchenko II, Romero MF, Schmitt BM;
AAW90262 standard; peptide; 1240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 5; 138pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                       97US-0047131
                                                                       (first entry)
                                                                                                             A. tigrinum AE2 protein.
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                                                                       27-APR-1999
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Sussman CR;
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                                 AAW90262;
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Gaps ö 66.1%; Score 74; DB 20; Length 1240; 65.0%; Pred. No. 0.026; 1ive 3; Mismatches 4; Indels ( Best Local Similarity 65.0 Matches 13; Conservative Query Match õ

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1 DRILLLEKPPKYHPDVPYVK 20

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Search completed: September 3, 2003, 11:46:13 Job time : 49.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-1 104 1 GMPWLSATTVRSVTHANALT 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hom	P23562 rattus norv	mus mus		7 oncorhy		P13808 mus musculu	P48746 oryctolagus		P16283 mus musculu			_		-	032962 mycobacteri	-	Q96q91 homo sapien	027083 methanobact	P51556 rattus norv	088673 mus musculu	008447 mycobacteri			Q10380 mycobacteri		4		P14176 escherichia	P23134 rhodospiril	_	8 caul	P04185 sus scrofa
SUMMARIES	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3AT_ONCMY	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	B3A2_CAVPO	B3A4_RABIT	LIPA_MYCLE	B3A4_RAT	B3A4_HUMAN	COBK_METTH	KDGA_RAT	KDGA_MOUSE	C13A_MYCTU	SL11_HUMAN	NU3M_HYLLA	LIPA_MYCTU	UROK_HUMAN	YKT5_SCHPO	NRFE_ECOLI	PROW_ECOLI	CYB_RHORU	KDGL_CAEEL	HEM3_CAUCR	UROK_PIG
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P11078 reovirus (t P20192 sus scrofa P42703 mus musculu P12915 b genome po 091210 mus musculu 09nyq7 homo sapien 088278 rattus norv P51208 porphyra pu P56938 rhodobacter P07519 hordeum vul P15321 serratia ma	
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WM2_REGVD KDGA_PIG LIFR MOUSE POLG_BOWEV CLR3_MOUSE CLR3_HUMAN CLR3_HUMAN YC56_PORPU YC56_PORPU CCDX_RHOSH CCB1_HORVU HLYB_SERWA	
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ALIGNMENTS

	RESU B3AT	RESULT 1 B3AT_HUMAN		ļ	ļ	,		
	TD AC	B3AT_HUMAN P02730:	STANDARD;	ARD;	PRT;	911 A	AA.	
	ī	21-JUL-1986	(Rel.	, Created)	_			
	r g	01-APR-1990	(Rel.	14, Last sec	sequence update)	pdate	~ `	
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	DE		antigen).	, (٠.
	S C	SLC4A1 OR AEI OR EPB3 OR DI	AEL OR EPB	3 OR DI.				
	88	Eukaryota;	Metazoa;	Chordata;		a; Ve	rtebrata; E	Craniata; Vertebrata; Euteleostomi;
	ဗ	Mammalia; Eutheria; Primates;	Eutheria;	Primates;		ini;	Catarrhini; Hominidae; Homo.	Ношо.
	X P	NCBI_TaxID=9606;	-9606;					
	RP	SEOUENCE FE	SOM N.A.					
	RX	MEDLINE=90083213; PubMed=2594752;	083213; Pu	bMed=25947	752;			•
	RA	Lux S.E.,	John K.M.,	Kopito R.	.R., Lod	ish H	.F.;	
	E E	"Cloning ar	nd charact	erization	of band	1 3, t	the human erythrocyte	ythrocyte anion-
	RI	Proc. Natl. Acad. Sci. U.S.A.	Acad. Sc	1. U.S.A.	86:9089-9093(1989)	-9093	(1989)	
_	RN	[2]					. (•
	RP	SEQUENCE FROM N.A.	ROM N.A.				•	
	RC	TISSUE-Blood;	og;					
	RX	MEDLINE=89134172; PubMed=3223947;	134172; Pu	bMed=3223	947;			
	RA	Tanner M.J.A., Martin P.G., High S.;	.A., Marti	n P.G., Hi	Lgh S.;	1	1	
	T.X.	Tue compile	ete amino	acid seque		the n	numan erythrocyte	ocyte memorane
	RI.	Blochem I 256:703-712/1988)	256.703-	712/1988)		o ann	DNA sequenc	י ט
_	N N	[3]		. (0001)21				
	RP	SEQUENCE OF	F 1-199; 2	20-292 ANE	347-37			
_	RX	MEDLINE=90001294; PubMed=2790053;	001294; Pu	DMed=27900	053;			
	RA	Yannoukakos	s D., Vass	eur C., Bl	louguit	Y., B	ursaux E.,	Wajcman H.;
	RT	"Primary st	tructure o	of the cytc	plasmic	doma:	in of human	erythrocyte
	KI.	procein bar	nd 3. comp	arison wit	CD 115 5	equen	ce in the m	procein band 3. Comparison with its sequence in the mouse."; Blockim Blockys Acts 608.43-40/1680.
	RN	[4]	topula. ur	C# . 0 . 0 . 10 .	000100			
	RP	SEQUENCE OF	F 1-201.					
	RX	MEDLINE-83238395; PubMed-6345535;	238395; Pu	1bMed=63455	535;			
	RA	Kaul R.K.	Murthy S.	N.P., Redc	dy A.G.,	Stec	k T.L., Koh	
	E E	"Amino acid	d sequence	of the N	alpha-t	ermin	"Amino acid sequence of the N alpha-terminal 201 residues of	residues of human
	RI.	T Biol C	hem 258.7	Chem 258:7981-7990/1983)	1983)			
	RN				. / 22 .			
	RP	SEQUENCE OF 1-3	F 1-3.					
	RX	MEDLINE-79027186; PubMed-701248;	027186; Pu	ibMed=70124	18;			
	RA	Drickamer L.K.;	L.K.;			,		
	RT	"Orientation	on of the	band 3 pol	Iypeptid	le tro	"Orientation of the band 3 polypeptide from human erythrocyte	throcyte
	T L	Garbohadrat	TOEHLILL	acton of r	1127 - 2HK	TINGT	sednence an	מ אורב סו
	RL	J. Biol. Chem. 253:7242-7248(1978)	hem. 253:7	242-7248(1	1978).			
	RN	[9]						
	RP	SEQUENCE OF 559-630.	F 559-630.	,	į			
_	RX	MEDLINE=83308584; PubMed=6615451;	308584; Pu	1bMed=66154	151;			
_	KA FG	##ho human	, Tanner r	1. J. A. , NE	npi C.,	+	Brock C.J., Tanner M.J.A., Kempi C.; #The human exerthrocute anion-transmort protein Dartial	Cipe Odine le
-	77	יווב יותוימיי	er y curocy	רב מוודמיי	Llansbor	יועי	CETTI FALLE	מד מוודווס מכזה

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us-10-087-464-1.rsp

PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE=20400020; Pubbed=10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E., Pina L.A., Donella-Deana A.;
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MEDLINE-92107882; PubMed-1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis."; VARIANT HE 400-ALA--ALA-408 DEL.
BEDLINE-S216721; bubmed-1538405;
Schofield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M., Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Okubo K., Hamasaki N., Hara K., Kageura M.;
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domain of erythrocyte band 3 protein associated with spherocytic
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MEDLINE-95134893; PubMed=7530501;
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the Diego (Dia) blood group antigen are associated with the human
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Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
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Lipoprotein;
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B3AT_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                           Kudrycki K.E., Shull G.E.;
Submitted (XXX-1992) to the EMBL/Genbank/DDBJ databases.

Submitted (XXX-1992) to the EMBL/Genbank/DDBJ databases.

IFUNCTION: BAND 3 HAS TWO FUNCTIONBL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPHASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).

SUBUNIT: A DIMBR IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
                                                                                                                                                                                                                                                                                                                                   Kudrycki K.E., Shull G.E., "Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
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          Length 911;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Kidney.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
           DB 1;
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         Score 104; DF
Pred. No. 4.36; Mismatches
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IsoId=P23562-1; Sequence=Displayed;
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HSSP; P02730; 1BTS.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                             deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
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EMBL; L02943; AAA40801.1; -.
                                                                      720 GMPWLSATTVRSVTHANALT 739
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MEDLINE=89255254; Pubmed=2722777;
                                                          1 GMPWLSATTVRSVTHANALT 20
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PRINTS; PR01231; HCO3TRNSPORT.
         Query Match 100.0%; Some Sest Local Similarity 100.0%; Promatches 20; Conservative 0;
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                                                                                                                                                                                                                                                                                             SEQUENCE OF 46-927 FROM N.A.
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                                                                                                                                                STANDARD;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
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PALMITATE (BY SIMILARITY).
Missing (in isoform Kidney).
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                                                                                                                                                       EXOPLASMIC LOOP (POTENTIAL)
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                CYTOPLASMIC (PÓTENTIAL).
MEMBRANE (ANION EXCHANGE).
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"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 104; DB 1;
Pred. No. 4.4e-09;
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splicing
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MEDLINE-85268011; Pubmed-2410791;
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MEDLINE-86034211; PubMed-3840489;
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Nature 316:234-238(1985).
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P04919;
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                                                                                                                                                                                                                                                           IsoId=P04919-2; Sequence=VSP_000454;
TISSUE SPECITITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                           SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC. SUBCELLULAR LOCATION: Integral membrane protein.
                                                         SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed=2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.;
Cioe L., Rovera G., Curtis P.J.;
Cloining and structural characterization of a human non-erythroid band 3-1ike protein.":
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PSO0219; ANION EXCHANGER_1; 1.
PROSITE; PSO0220; ANION EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXOPLASMIC LOOP (POTENTIAL)
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                                                                                                                                                                                                                       Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
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HSSP; POO730; IBTS.
MGD; MGT:109393; S1c4a1.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PP00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                            EMBL; X02677; CAA26506.1; -. EMBL; M02979; AAA37187.1; -. EMBL; X02556; AAA37278.1; -. EMBL; X03917; CAA27555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FIGRFAMS; TIGRO0834; ae; 1
                                                                                                                                                                                                             ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643
                                                                                                                                                                                                                                                   Name-Kidney
                                                                                      Passow H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
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-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: ERYTROCYTE.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACROSS
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01-APR-1990 (Rel. 14, Last sequence update)
01-FBP-1996 (Rel. 33, Last annotation update)
Band 3 anion transport protein.
Gallus gallus (Chicken).
Ebwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                         Length 929;
                                            Missing (in isoform Kidney).
/FTId=VSP_000454.
6 - S (IN REF. 5).
5 5C0E281C394FB614 CRC64;
                                                                                                                                                                                                                                                                                                                     Indels
        PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                         100.0%; Score 104; DB 1; 100.0%; Pred. No. 4.4e-09;
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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MEDLINE-89039870; PubMed=3185555;
                                                                                                                                                                                                                                                                                                                                                                                                                                      738 GMPWLSATTVRSVTHANALT 757
                                                                                                                                                                                                                                                                                                                                                                                          1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
861
79
                                                                                                                        467
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929 AA;
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Matches 20; Conserv
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450
473
504
536
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ID B3AT_CHICK
AC P15575;
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TRANSMEM
TRANSMEM
                                        VARSPLIC
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                                                                                                                        CONFLICT
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EMBL; J05166; AAA40799.1; -.
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                                                                                                                                                                                                                             918 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rissue=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopito R.R.;
                                                                                                                                                                                                     CARBOHYD
               TRANSMEM
                                                                                                     FRANSMEM
                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                         Query Match
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                                                                            TRANSMEM
                                                                                                                             PRANSMEM
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   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-9234456; PubMed=1637296;
A Hubner S., Michel F., Rudloff V., Appelhans H.;
Hubner S., Michel F., Rudloff V., Appelhans H.;

"Amino acid sequence of band-3 protein from rainbow trout
ry erythrocytes derived from cDNA.";
Blochem. J. 285:17-23(1992).

"I EVGNION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
HEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKEDETALA AND OTHER PROTEINS (BY SIMILARITY).

"CONTOCKEDETAL AND OTHER PROTEINS (BY SIMILARITY).

"CONTOCKED AND APPEARS TO BE TETRAMBRIC (BY SIMILARITY).

"CONTOCKED AND APPEARS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                         ö
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate.
DOMAIN 1 392 CYTOPLASMIC (POTENTIAL).
DOMAIN 393 918 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                           N-LINKED (GLCNAC. . .) (PROBABLE).
MW; FF4ECAD6D60CF0CF CRC64;
                                                                                                                                                                                           ö
                                                                                                                                                                Score 100; DB 1; Length 922;
EXOPLASMIC LOOP (POTENTIAL)
                                      POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                        0; Indels
                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                            2e-08;
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Last annotation update)
                                                                                                                                                                                         2; Mismatches
                                                                                                  POTENTIAL. POTENTIAL.
                                                               POTENTIAL.
                                                                           POTENTIAL.
                                                                                        POTENTIAL.
                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            731 GMPWLSATTVRTITHANALT 750
                                                                                                                                                                                                                 1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                            01-0CT-1993 (Rel. 27, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                  Band 3 anion exchange protein.
                                                                                                                                                               96.2%;
90.0%;
                                                                                                                                         102223
                                                                                                                                                                            Local Similarity 90.0 es 18; Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                  671
691
730
791
                                                                                                                                       922 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                SLC4A1 OR AE1.
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P32847;
                       DOMAIN
TRANSMEM
 DOMAIN
TRANSMEM
                                                DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                           CARBOHYD
                                                                                                                                       SEQUENCE
                                                                                                                                                                  Query Match
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Matches
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or send an email to license@isb-sib.ch)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                    974 POTENTIAL.

552 PALMITATE (BY SIMILARITY).

546 N-LINKED (GLCNAC. . ) (POTENTIAL).

568 N-LINKED (GLCNAC. . ) (POTENTIAL).

101893 MW; 37E163141FBDC16A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 918;
                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.3e-07;
Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLUTAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1234 AA.
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                                                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                          POTENTIAL.
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MEDLINE=90094439; PubMed=2294114;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%;
90.0%;
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Matches 18; Conservative
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Name=C1;
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TRANSMEM
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VARSPLIC
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                  <u>+</u>.
Gaps
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P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, created)
28-FEB-2003 (Rel. 13, Last sequence update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AB2.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A).
MEDGLINE-89034212; PubMed=3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE-20462926; Pubmed-11006093; Lecanda J., Urtasun R., Medina J.F.; "Molecular cloning and genomic organization of the mouse AE2 anion
  HISP: P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
InterPro; IPR00351; HCO3_TRNSPORT.
TIGRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                Score 93; DB 1; Length 1234;
                                                                                                                                                          EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               Score 93; July Pred. No. 3.7e-07;
Pred. No. 3.7e-07;
                                                                                                                                                                                                                                   PRO-RICH.
HIS-RICH.
N-LINKED (GLCNAC. . .) (POTH
N-LINKED (GLCNAC. . .) (POTH
N-LINKED (GLCNAC. . .) (POTH
PALMITARE (BY SIMILARITY).
G -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                    > I (IN REF. 2).
FAB4ED12BB916216 CRC64;
                                                                                                    CYTOPLASMIC (POTENTIAL). MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 276:117-124(2000).
                                                                                                                                                                                                                                                                                                           -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                  (IN REF.
                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                        POTENTIAL.
                                                                                                                                POTENTIAL.
                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                    -> PG
                                                                                                                                                                                                                                                                                                                                                                                               1043 GLPWLAAATVRSVTHANALT 1062
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                                                                                                                                                                                                                                                                                                                                                                                    1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                               89.4%;
                                                                                                                                                                                                                                                                                                                               136635
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 85.0
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                    1156 11:
1234 AA;
PIR; A34911; A34911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchanger
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                             DOMAIN
TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                     FRANSMEM
                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                               TRANSMEM
                                                                                                                                                 TRANSMEM
                                                                                                                                                                                        FRANSMEM
                                                                                                                                                                                               FRANSMEM
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                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stommach although they are also detected at lower levels in other tissues. Isoform c1 is stommach-specific. Isoform c2 is expressed at slightly higher levels in lung and stommach than in other tissues. SIGNIANTY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALMITATE (BY SIMILARÍTY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Antion exchange; Lipoprotein; Palmitate; Alternative splicing. DOMAIN 1 CYTOPLASMIC (POTENTIAL).

MEMBRAIN 704 . 1237 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                     SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GLCNAC. . .)
                                                                                                                               Event=Alternative splicing; Named isoforms=5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B2).
/FTId-VSP_000457
                                                                                                                                                                                                                                                                                                                      IsoId=P13808-3; Sequence=VSP_000457;
                                                                                                                                                                                                                                                                                                                                                                                      IsoId-P13808-4; Sequence-VSP_000460;
                                                                                                                                                                                                                                                          IsoId=P13808-2; Sequence=VSP_000458;
                                                                                                                                                                                           IsoId=P13808-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR01171; Anion_exchange.
InterPro; IPR01302; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF255774; AAG23154.1; -.
EMBL; AF255774; AAG23155.1; -.
EMBL; AF255774; AAG23156.1; -.
EMBL; AF255774; AAG23158.1; -.
EMBL; AF255774; AAG23157.1; -.
PIR; A31789; A31789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J04036; AAA65505.1; -.
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TRANSMEM
DOMAIN
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                             TRANSMEM
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 DOMAIN
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                                                                                                                                         LIPID
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                                                                                                                                                  ö
                                               /FTIG-VSP_000460.
ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
GLREEAVFGAHGCSVCR (in isoform C2).
MSSAPRRPASGADSLHT -> MTQ (in isoform B1).
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane: Glycoprotein; Transport; Antiport; Ion transport; Anion exchange: Lipoprotein; Palmittete.

CYTOPLASMIC (POTENTIAL).

DOMAIN 704 1237 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-New Zealand white;
MPDLINE-93035730; Pubmed-1415547;
Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"Chow A., Cobbins J.W., Aronson P.S., Igarashi P.;
                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Am. J. Physiol. 263:G345-G352(1992).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                             Length 1237;
                                                                                                                                                  1; Indels
                                                                               /FTIG-VSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
         /FTId=VSP_000458.
Missing (in isoform C2).
                             /FTId=VSP_000459.
Missing (in isoform C1).
                                                                                                                           DB 1; L
3.7e-07;
                                                                                                                                                                                                                                               PRT; 1237 AA.
                                                                                                                           Score 93; DB 3.7e. Pred. No. 3.7e. 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL. POTENTIAL.
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InterPro: IPR001717; Anion_exchange.
InterPro: IPR003020; HCO3_cotranspt.
Pfam: PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                 1046 GLPWLAAATVRSVTHANALT 1065
                                                                                                                                                                     1 GMPWLSATTVRSVTHANALT 20
                                                                                                       136813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; $45791; AAB23488.1; -. PIR; A56764; A56764.
                                                                                                                           89.4%;
                                                                                                                    Ouery Match
Best Local Similarity 85.09
                                                                                                                                                                                                                                               STANDARD;
                                        198
                    166
                                                                                             205
                                                            193
                                                                                           205 20
1237 AA;
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9986;
                                                            167
                                                                                                                                                                                                                                                                                                                SLC4A2 OR AE2
                                                                                                                                                                                                                                               B3A2_RABIT
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A MEDLINE-22388257; PubMed=12477932;

Ratausher R.D., Collins E.A., Grouse L.H., Derge J.G.,

Ratausher R.D., Collins E.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rataled S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Ratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Ratchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Ratchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Ratcherton M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,

Ratching M., Madan A., Sodergren E.J., Lu X., Gibbs R.A.,

Rahy T., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Ratkseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ratkseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ratkseley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Ratching A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.;

Ratherfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Rather and mouse cond. Schmutz J., Marra M.A.;

Rhuan and mouse cond. Schmutz J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B3A2_HUMAN STANDARD; PRT; 1241 AA.
P04230; 03969L3;
13-AGG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AEZ OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 375-1241 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
                                                                                                                                                                                                                                                                                                              | N-LINKED (GLCNAC. . .) (POTENTIAL).
| N-LINKED (GLCNAC. . .) (POTENTIAL).
| N-LINKED (GLCNAC. . .) (POTENTIAL).
| PALMITATE (BY SIMILARITY).
| 136535 MW; 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93; DB 1; Length 1237;
Pred. No. 3.7e-07;
2; Mismatches 1; Indels
  EXOPLASMIC LOOP (POTENTIAL)
                                               CYTOPLASMIC (POTENTIAL). POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochim. Biophys. Acta 1130:326-328(1992)
                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
PRO-RICH.
HIS-RICH.
                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein AE2 from human kidney.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.4%;
85.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.0°
896
914
929
929
1006
11053
11132
11195
316
88
855
864
878
878
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                                                                                                                                        1032
1087
1159
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                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                             TRANSMEM
TRANSMEM
TRANSMEM
TRANSMEM
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450
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                                                                                                                                                                                                                                                                                                      B3A3_MOUSE
P16283;
                                                                                                  CONFLICT
                                        CONFLICT
             CONFLICT
                                                                                    CONFLICT
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                         B3A3_MOUSE
                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                       SILLLLES
                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mee by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALMITATE (BY SIMILARITY).
MSSAPRLPAKGADSFCT -> MTQ (in isoform B1).
                                                                                                                                                                                                                                                                                                                                                      | REMEL; X62137; CA444067.1; -
| REMEL; BC009386; AAH09386.1; -
| REMEL; BC009344; AAH09434.1; -
| REMEL; BC009444; AAH09434.1; -
| REMEL; MC09186; CA27556.1; -
| REMEL; X03918; CA27556.1; -
| REMEL; X03918; CA27556.1; -
| REMEL; X03918; CA427556.1; -
| REMEL; X03918; CA427556.1; -
| REMEL; X03918; CA42.
| REMEL; MCC: 1028; SLC442.
| REMEL; MCC: 1028; SLC442.
| REMEL; MCC: 1028; SLC442.
| REMEL; RC: 1028; SLC442.
| REMERRARE; SLC442.
| RC: 1028; SLC442.
Cioe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid band 3-like protein.";
EMBO J. 5:1205-1214(1986).
-i- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).

N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                    ISOId=P04920-2; Sequence=VSP_000456; SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                              Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> M (IN REF. 1
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                                                                                                                                                                        IsoId=P04920-1; Sequence=Displayed;
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1241 M
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                                                                                                                                                                                                                                                                                         ö
LLGHHHGQGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                     VTPTSPSLSWEVFLR (IN REF. 3).
EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                                                                         Gaps
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed=2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.
                                                                                                                                                                                                                                                                                         ö
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MEDLINE-94171936; Pubmed-8126106;
Morgans C.W., Kopito R.R.;
Generation of truncated brain AE3 isoforms by alternate mRNA processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schneider K.;
"Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger.";
cell 59:927-937(1989).
                                                                                                                                                                                                                                   Score 93; DB 1; Length 1241; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
-!- TISSUE SPECIFICITY: NEURONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1227 AA
                                                                                                                                                                                                                                                                                   2; Mismatches
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IsoId=P16283-1; Sequence=Displayed;
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HSSP, P02730, IBTO,
MGD; MG1.109350; Slc4a3.
InterPro; IPR001717; Anion_exchange.
                                                                                                                                                                                                                                                                                                                                                                    1050 GLPWLAAATVRSVTHANALT 1069
                                                                                                                                                                                                                                                                                                                                            1 GMPWLSATTVRSVTHANALT
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                                                                                                                                                                                  136966
                                                                                                                                                                                                                                     89.4%;
85.0%;
                                                                                                                                                                                                                                                                                         Conservative
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                                                486
                                                                                                                            824
                                                                                                                            824 82
902 90
1241 AA;
                                                                                                                                                                                                                                                        Local Similarity
es 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=14-AE3
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1232 AA.
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POLY-LYS.
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                                                     EMBL; J05167; AAA40798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                135406
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80.0%;
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Best Local Similarity 80.0.
The conservative
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868
1160
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1182
                                                                 PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                            HSSP; P02730; 1BTQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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P48751;
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SEQUENCE
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                                                                                                                                                                                                                                                                              /FTIGHOVSP_000464.
Missing (in isoform 311-AE3).
FTIGHOVSP_000465.
KPLHWPGGDGHRGKSIK -> FCVLRSPSPCLGETVTEGKA (in isoform 14-AE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostom1;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90094439; PubMed=2294114;
MEDLINE-90094439; PubMed=2294114;
Kudrycki K.E., Newman P.R., Shull G.E.;
CDNA cloning and tissue distribution of mRNAs for two proteins that are related to the band 3 C1-/HCO3-exchanger.";
J. Blol. Chem. 265:462-471(1990).
I- FUNGTION: PLASMA MEMBRANE ANTON EXCHANGE PROTEIN.
--- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                             AALLDLEQTTL -> RAFWAGNESLL (in isoform
                                                              Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                           Length 1227;
                                                                                                                                                                                                                                                                                                                                                                                Score 89; DB 1; Length 122
Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                  Missing (in Isoform 14-AE3).
                                                                                                                                                                                                                                                                                                                                                          FTId=VSP_000467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AB3 OR B3RP3.
Rattus norvegicus (Rat).
                                                                                               MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- TISSUE SPECIFICITY: NEURONAL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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PALMITATE (BY SIMILARITY)
                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                       FTId=VSP_000466
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                                                                                      CYTOPLASMIC
                                                                                                                                                                        POTENTIAL. POTENTIAL.
                             TICRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                          POTENTIAL.
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                                                                                                           POTENTIAL.
                                                                                                                               POTENTIAL.
                                                                                                                                                                                                         POTENTIAL
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1037 GLPWLTAATVRSVTHVNALT 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GMPWLSATTVRSVTHANALT 20
                                                                                                                                                                                                                                                                                                                                                                     1227 AA; 135164 MW;
                     PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                           85.6%;
80.0%;
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                                                                                                                                                                                                                                                                                                                 503
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es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                 504
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Gardiac/brain band 3-like protein) (CAE3/BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                            TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transsmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
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MEDLINE-55008042; PubMed-7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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Pred. No. 1.6e-06;
2; Mismatches 2; Indels
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W; 3EB1620EE011730E CRC64;
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                 Kudo S., Mattel M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                                                         ISOId=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00119; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -> MPA (in isoform CAE3).
                                                                                                                                                                                                                                                                                                                                                              G0:0005887; C:integral to plasma membrane; TAS. G0:0005624; C:membrane fraction; TAS. G0:0005452; F:inorganic anion exchanger activity; TAS. G0:0006832; P:small molecule transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Missing (in isoform CAE3)./FTId=VSP_000462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                VENTRICLE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                 SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                            ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms-2;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> V (IN REF. 2).
                                                                                                                                     IsoId=P48751-1; Sequence=Displayed;
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POTENTIAL.
POLY-GLU.
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                                                                                                                                                                                                                                                                                                                                                              GO; GO:0005887; C:integral to plasma me GO; GO:0005624; C:membrane fraction; TR GO; GO:0005452; E:inorganic anion exchisco; GO:0006832; P:snall molecule transf InterPro; IPR001717; Anion exchange: InterPro; IPR001707; Anion exchange: Pfam; PF00955; HGO3_cotranspt. Pfam; PF00955; HGO3_cotranspt.
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POLY-LYS.
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SEQUENCE FROM N.A. (ISOFORM CAE3).
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EMBL; L27213; AAB05850.1; -.
PIR; 138496; 138496.
HSSP; P02730; 1BTQ.
Genew; HGNC:11029; SLC4A3.
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                                                                                                                            Name=BAE3;
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        rissum=Heart;
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGRRAMS; TIGR00834; ae, 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion
                                                                                                                                                                                                                                                                                          Length 1232;
                                                                                                                                                                                  > E (IN REF. 2).
> P (IN REF. 2).
> M (IN REF. 2).
1825BE15977C3821 CRC64;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abuladze N., Pushkin A., Kurtz I.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: NEDRONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                         REF. 2).
IN REF. 2).
REF. 2).
REF. 2).
                                                                                                             REF. 2).
(IN REF. 2)
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P -> S (IN REF
S -> G (IN REF
DS -> F (IN REF
F -> L (IN REF
A -> S (IN REF
GSIA -> D (IN
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S -> G (IN REF
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
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1042 GLPWLTAATVRSVTHVNALT 1061
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                                                                                                                                                                                                                                                                                          85.6%;
80.0%;
                                                                                                                                                                                                                                                   1232 AA; 135706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exchanger 3 brain isoform).
                                                                                                                                                                                                                                                                                                             Local Similarity 80.0 les 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9986;
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738
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827
894
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018917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsuganezawa H., Kobayashi K., Iyori M., Araki T., Koizumi A., Watanabe S.-I., Kaneko A., Fukao T., Monkawa T., Yoshida T., Kim D.K., Kanai Y., Endou H., Hayashi M., Saruta T.;
A new member of the HC03-transporter superfamily is an apical anion exchanger of beta intercalated cells in the kidney.";
J. Biol. Chem. 276:8180-8189(2001).
I-FUNCTION: Probable apical anion exchanger of the beta-intercalated cells of kidney. May participate in HC03(-) secretion.

-: SUBCELLULAR LOCATION: Integral membrane protein. In contrast to the call of kidney, May periodipate in HC03(-) secretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=AE4b;
IsoId=Q9GKY1-2; Sequence=VSP_007088;
-!- TISSUE SPECIFICITY: Highly expressed in kidney. Expressed in certain types of cells in the kidney cortex.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
PALMYTATE (BY SIMILARIY).
W; FA1739862ED5ADBF CRC64;
                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                  Score 83; DB 1; Length 1238;
Pred. No. 1.6e-05;
2; Mismatches 2; Indels
         POTENTIAL.
POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney cells.
-!- ALTERNATIVE PRODUCTS:
    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 4 (Anion exchanger 4).
CLGA9 OR AE4.
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                        955 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=1; Synonyms=AE4a;
IsoId=Q9GKY1-1; Sequence=Displayed;
                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
PRO-RICH.
                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21269379; PubMed=11102437;
                                                                                                                                                                                                                                                                                                                           1 GMPWLSATTVRSVTHANALT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                    B3A4_RABIT STANDARD;
Q9GKY1; Q9GKY2;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last seq.
15-SEP-2003 (Rel. 42, Last seq.
                                                                                                                                                                                                                                                                     79.8%;
80.0%;
                                                                                                                                                                                                                                            137358
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Best Local Similarity 80.v.
These 16; Conservative
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930
951
1007
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                               10-UCI-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prince, invocation hous_corranspt.

Prims: Pr00955; HCO3_corransp; 1.

PR1012; PR01231; HCO3TRNSPORT.

TIGREAMS; TIGRO084; as: 1.

PROSITE; PS00219; ANION_EXCHANGER_1; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.

Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.

DOMAIN 1 TOP CYTOPLASMIC (POTENTIAL).

DOMAIN 705 1238 MEMBRANE (ANTON FYCHANGE).
                                                                             (POTENTIAL)
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                                                                                                                                                                                                                 Length 1233;
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Pred. No. 1.6e-06;
                                                                                                                                                                                      AE486423E9818583 CRC64;
                                                                             N-LINKED (GLCNAC. . .) (PO
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
CYTOPLASMIC (POTENTIAL).
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                                                  POTENTIAL. POTENTIAL.
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POLY-GLU.
                                       POTENTIAL
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InterPro; IPR003020; HCO3_cotranspt.
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                                                                                                                                                                                       AA; 135759 MW;
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16-0CT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
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Q9Z0S8;
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Matches
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or send an email to license@isb-sib.ch).
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                                                                                                      HSSP; P02730; 1BNX.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003171; Anion_exchange.
InterPro; IPR003020; HC03_cotransp.
Pfan; PF00955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TRGRRAMs; TGR00834; ac, 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXOPLASMIC LOOP (POTENTIAL)
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871 891 POTENTIAL.

548 548 N-LINKED (GLCNAC. . .) (POT

572 572 N-LINKED (GLCNAC. . .) (POT

317 332 Missing (in isoform 2).

/FTId=VSP_007088.

955 AA; 105032 MW; 04E595A2BFC415B7 CRC64;
                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
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Best Local Similarity
Matches 8; Conserva
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CARBOHYD
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Search completed: September 3, 2003, 11:46:55 job time: 10.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-2 98 1 SVTHANALTVMGKASTPGAA 20 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P02730 homo sapien	ratto	PO4919 mus musculu	P23347 rattus norv	P13808 mus musculu	P48746 oryctolagus		homo sa	P15575 gallus gall	oncorh	P16283 mus musculu	P23348 rattus norv	P48751 homo sapien	-			P14914 rickettsia	Q53047 r outer mem				Q02482 shewanella	Q8uey3 agrobacteri	-	P33025 escherichia	Q92210 candida alb	Q10821 mycobactéri	Q61140 mus musculu	7	P54189 plasmodium	œ	118 cephalos	P46596 candida alb
SUMMAKIES	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3AT_CHICK	B3AT_ONCMY	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	Y003_HAEIN	OMPB_RICCN	120K_RICRI	OMPB_RICRI	NUCL_HUMAN	FTSY_RICPR	WD21_HUMAN	YFC5_SHEFR	TPIS_AGRT5	PANB_OCEIH	YEIN_ECOLI	PUR6_CANAL	YTOO_MYCTU	BCA1_MOUSE	BCA1_RAT	PBP_PLAFA	BRS3_MOUSE	ALP_CEPAC	OPS4_CANAL
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ALIGNMENTS

RESULT 1 B3ATHUMAN ID B3ATHUMAN ID B3ATHUMAN ID B3ATHUMAN ID B3ATHUMAN ID B1-AP DT 01-AP DT 0
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Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,
Pinna L.A., Donella-Deana A.;
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MEDLINE-92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast
Asian ovalocytosis.";
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MEDLINE=92167271; PubMed=1538405;
Schoffield A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M.,
Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M.,
Gratzer W.B.;
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sequence, conformation and a possible molecular mechanism for anion
                                                             MEDIINE-88228050; PubMed-3372523;
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terminal region of erythrocyte band 3 protein.";
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"Palmitoylation of cysteine 69 from the COOH-terminal of band 3 protein in the human erythrocyte membrane. Acylation occurs in t middle of the consensus sequence of F-I-IICLAVL found in band 3 protein and G2 protein of Rift Valley fever virus.";
J. Biol. Chem. 266:16420-16424(1991).
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Jarolim P., Palek J., Rubin H.L., Prchal J.T., Korsgren C.,
                                                                                                                                                                                                                                                                                                                                                              PHOSPHORILATION OF TYR-8; TYR-21; TYR-359 AND TYR-904 MEDLINE-20400020; PubMed-10942405;
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                                                                                                                                              ROLE OF GLU-681, AND SEQUENCE.OF 665-688.
MEDLINE=92332495; PubMed=1352774;
                                                                                                                                                                                                                                                                                                                                                                                                                                             secondary phosphorylation sites.";
Blood 96:1550-1557(2000).
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MEDLINE=91358422; PubMed=1885574;
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MEDLIŅE-93343855; Pubmed-8343110;
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[15]
                       Biochem. J. 213:577-586(1983)
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                                                     OF 834-911.
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               exchange
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VARIANTS HS GLN-760; TRP-760; CYS-808 AND TRP-870.
MEDLINE=95134893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
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the membrane domain of band 3.";
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MEDLINE-96136073; PubMed-8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Maillet F., Tanner M.J., Delaunay J., Alloisio N.;
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spherocytosis and substitution in a highly conserved position of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.

WEDLINE-94266802. PubMed-8206915.

Bruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;

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J. Biol. Chem. 269:16155-16158(1994).
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BEDLINE-96254540; PubMed-8640229;

EDER S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,

Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,

Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
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Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozor
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
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                                                                                                                                                                                                                                                                                              MEDLINE-93229758; PubMed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
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MEDLINE=95111140; PubMed=7812009;
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                                                                                                                                                                                                                                                          VARIANT MONTEFIORE LYS-40
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Blood 85:541-547(1995).
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SLC4A1 OR AE1
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P04919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kudrycki K.E., Shull G.E.,
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
-!-SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
COLLECTING DUCTS.
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kudrycki K.E., Shull G.E.; "Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SIC4A1 OR AE1.
                                                           ;
                Length 911;
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PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00084; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: Event-Alternative splicing; Named isoforms-2;
                Score 98; DB 1; 1
Pred. No. 1.5e-08;
Mismatches 0;
                                                                                                                                                                                                                                             927 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Kidney;
IsoId=P23562-2; Sequence=VSP_000455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Erythrocyte;
IsoId=P23562-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deduced from a cDNA.";
J. Biol. Chem. 264:8185-8192(1989).
                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J04793; AAA40800.1; ALT_INIT
EMBL; L02943; AAA40801.1; -.
                                                                                               100.0%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89255254; PubMed=2722777;
                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 46-927 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-45 FROM N.A.
                                                         Conservative
                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
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                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P02730; 1BTS
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                         20;
                                                                                                                                                                                                                                             B3AT_RAT
                                                         Matches
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                                                                                                                                                                                                    RESULT 2
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Kopito R.R., Lodish H.F.; "Primary structure and transmembrane orientation of the murine anion exchange protein.": Nature 316:234-238(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (PROBABLE)
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB 1; Length 927; Pred. No. 2.2e-07;
               CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
POTENTIAL.
POTENTIAL.
                                                                                                                        POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A.
MEDLINE-87250387; PubMed-3036795;
KOpito R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                   POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform Kidney) /FTId=VSP_000455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     681A228474E5E9DE CRC64;
                                                                                                                                                                                         POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-66034211; Pubmed-3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
J. Cell. Biochem. 29:1-17(1985).
Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        929 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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MEDLINE=86274622; PubMed-3015590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103172 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.9%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
Palmitate:
                                                                                                                                                                                                                                                                                                735
796
822
881
658
859
79
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                                                                                                                                                                                after in situ proteolysis.",
Biochim. Biophys. Acta 980:291-298(1989).
-! FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
-! FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE
ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS
INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANYONS ACROSS
THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                 SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPERARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                  Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                                    Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e; Glycoprotein; Anion exchange; Erythrocyte; Palmitate; Alternative splicing.
1 422 CYTOPLASMIC (POTENTIAL).
123 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXOPLASMIC LOOP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: ERYTHROCYTE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  Event-Alternative splicing; Named isoforms-2;
                                                                                                   SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP, P02730, 1BTS.
MGD; MGI:109393; S1c4a1.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRRAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId-P04919-2; Sequence-VSP_000454;
                                                                                                                                                                                                                                                                                                                                                                                                 Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                 MEDLINE-89229233; PubMed-2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X02677; CAA26506.1; -. EMBL; M29379; AAA37187.1; -. EMBL; 102756; AAA37278.1; -. EMBL; X03917; CAA27555.1; -. PIR; A25314; A25314;
                                                   band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipoprotein;
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TRANSMEM
CARBOHYD
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                                                                                                                                                    ö
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enkaryotė; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kudrycki K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl./RCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                                                                                        01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Transmembrane; Clyporotein; Palmitate.

DOMAIN 705 1234 MEMBRANE (ANION EXCHANGE).

TRANSMEM 705 728 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional expression and subcellular localization of an anion
                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90319095; Pubmed-2371270;
Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                92.9%; Score 91; DB 1; Length 929; 95.0%; Pred. No. 2.2e-07;
                     Missing (in isoform Kidney). /FTId=VSP_000454.
                                                                                                                                                    1; Indels
                                                        467 G -> S (IN REF. 5).
103135 MW; 5C0E281C394FB614 CRC64;
   PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                         PRT; 1234 AA.
                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90094439; Pubmed=2294114;
                                                                                                                                                                                                                              SVTHANALTVMGKASGPGAA 768
                                                                                                                                                                                       1 SVTHANALTVMGKASTPGAA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J05166; AAA40799.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR00834; ae;
                                                                                                                                 Best Local Similarity 95.0 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                         STANDARD;
861
79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A34911; A34911.
                                                          467
929 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kopito R.R.;
                   VARSPLIC
                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                         B3A2_RAT
                                                                                                                Query Match
                                                          CONFLICT
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          -:- TISSUE SPECIFICITY: İsoform a İs widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform cl is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PALMITATE (BY SIMILARITY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                                                                                                                                                                HSSP; PU2/34; 151.4.
MGD; MGI:109351; 31.4.
MGD; MGI:109351; 31.4.
InterPro; IPR0013020; HGO3_cotranspt.
Pfam; PR00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORT.
TIGREAMS; TIGR0034, a.a.; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Transmembrane; Liboprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 · · · (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VSP_000457.
MSSAPRRPASGADSLHT -> MTQ
IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform C2)./FIId=VSP_000459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Missing (in isoform C1). /FTId=VSP_000460.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-SER.
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
N-LINKED (GLCNAC..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 73; DB 1; Pred. No. 0.00033;
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                                                                                                                                                                                                                     EMBL; J04036; AAA65505.1; -.
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P13808; Q9ES09; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-89034212; PubMed-3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDIINE-20462926; Pubmed-11006093; Lecanda J., Urtasun R., Medina J.F.; "Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Biochem. Blochys. Res. Commun. 276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                                                                                Score 73; DB 1; Length 1234; Pred. No. 0.00033;
                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
PALMITATE (BY SIMILARITY).
G -> A (IN REF. 2).
RR -> PG (IN REF. 2).
                         POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                               M -> I (IN REF. 2).
M -> I (IN REF. 2).
MW; FAB4ED12BB916216 CRC64;
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                                                              CYTOPLASMIC (POTENTIAL)
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  Gaps
                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2.
                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ransmembrane; Glycoprotein; Transport; Antiport; Ion transport;
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STRAIN-New Zealand white;
MFDLIN-E93035730; Pubmed=1415547;
Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"CDNA Cloning and localization of a band 3-related protein from
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                                                                                                                                                                                                                                                                                    Am. J. Physiol. 263:G345-G352(1992).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
 Indels
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-i - SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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                                                                                           PRT; 1237 AA.
 Mismatches
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InterPro; IPR001317; Anion_exchange.
InterPro; IPR0013020; HC03_cotranspt.
Ffam; PP00955; HC03_cotranspt.
PRINTS; PR01231; HC03TRNSPORT.
TIGRAMS; TIGROMS31, as; 1.
FROSITE; PS00139; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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                              SVTHANALTVMSKAVAPG 1074
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                   SVTHANALTVMGKASTPG 18
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 Conservative
                                                                                             STANDARD;
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STRAINS-NIH 2; TISSUE-Organ of Corti;
STRAINS-190023787; pubmed-9804866,
Medithe 99023787; pubmed-9804866
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
"The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2 anion exchanger).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavildae; Cavia.
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-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                       Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXOPLASMIC LOOP (POTENTIAL).
                                                                                      Indels
136535 MW; 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: Integral membrane protein.
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                         Score 73; DB 1; Ler
Pred. No. 0.00033;
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HIS-RICH.
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
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HSSP; P02730; 1BTQ.
                                         74.5%;
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                                                                                        Conservative
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   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A MEDLINE-22388257; PubMed-12477932;

A Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Rlausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Both S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Brakesley S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Hitalon D.K., Muzny D.M., Scheune D.D., Dickson M.C.,
A Buakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Generation and initial analysis of more than 15,000 full-length
A Draw May M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. All M. Al
                                                                                                                                                                                                                                                                             B3A2_HUMAN STANDARD; PRT; 1241 AA.
P04920; Q969L3;
13-A0G-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AE2 OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
Cloe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
MW; FA1739862ED5ADBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                Length 1238;
                                                                                                 ) Db 1,
0.00033;
... 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein AE2 from human kidney.";
Biochim. Biophys. Acta 1130:326-328(1992)
                                                                                                 Score 73;
Pred. No. (
                                                                                                                                                                                  1058 SVTHANALTVMSKAVAPG 1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                 1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 375-1241 FROM N.A.
856 856
865 865
879 879
1170 · 1170
1238 AA; 137358 M
                                                                                                74.5%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     band 3-like protein.";
EMBO J. 5:1205-1214(1986)
                                                                                                               Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain
CARBOHYD
CARBOHYD
CARBOHYD
LIPID
                                                                 SEQUENCE
                                                                                                   Query Match
                                                                                                                                                                                                                                                                 B3A2_HUMAN
                                                                                                                                                                                                                                                  RESULT 8
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@isb-sib.ch).
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
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MSSAPRLPAKGADSFCT -> MTQ (in isoform Bl).

//TIGH-VSP_000456.

E -> M (IN REF. 1).

H -> R (IN REF. 1).

C -> R (IN REF. 1).

C -> R (IN REF. 1).

E -> V (IN REF. 1).

E -> V (IN REF. 1).

L -> V (IN REF. 1).

L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L -> V (IN REF. 1).
LLGHHHGQGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Palmitate; Alternative splicing.
CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1241;
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POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                       IsoId-P04920-2; Sequence=VSP_000456; SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIPISPSLSWEVFLR (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 109280; -. Geombrane fraction; TAS. GO; GO:0005624; C:membrane fraction; TAS. GO; GO:0008509; F:anion transporter activity; TAS. GO; GO:0006820; P:anion transport; TAS.
IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO1231; HCG3TRNSPORT.
TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE: PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotransp; 1.
                                                                                                                                                                                                                                                                        EMBL; X62137; CAA44067.1; -.
EMBL; BC009386; AAH09386.1; -.
EMBL; BC009434; AAH09434.1; -.
EMBL; X03918; CAA27556.1; -.
PIR; S21086; S21086.
HSSP; P02730; IBTQ.
Genew; HGNC:11028; SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anion exchange; Lipoprotein;
DOMAIN 1 707
DOMAIN 708 1241
TRANSMEM 708 731
TRANSMEM 737 774
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681
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902
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157
248
399
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902 90
1241 AA;
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TRANSMEM
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                                                               Query Match
                                   CARBOHYD
                                            SEQUENCE
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                                                                                                                                                    RESULT 10
B3AT_ONCMY
                                                                                  Matches
                                                                                                                                                                        SET
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                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                ö
                                                                                                                                                                                                                   SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                 Gaps
                                                                                                                                                                                                                                                                                                                   THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREAMS; TIGRO0834; ae; 1.
TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
CYTOPLASMIC (POTENTIAL).

A16
CYTOPLASMIC (POTENTIAL).

A22
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXOPLASMIC LOOP (POTENTIAL).
POTENTIAL.
POTENTIAL.
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                       AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL) POTENTIAL.
Pred. No. 0.00033;
                                                                                                                     01-APR 1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
and 3 anion transport protein.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINYS; PR01231; HCO3TRNSPORT.
                                            1061 SVTHANALTVMSKAVAPG 1078
               ö
                                 1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M23404; AAA48753.1; -.
     83.3%;
     Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                    STANDARD;
                                                                                                                                                                                                   NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                       HEMOGLOBIN.
                                                                                                 B3AT_CHICK
P15575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
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TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOCHEM. J. 285:17-23(1992).

-1- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOWAINS: ITS INTEGRAL DOWAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).

-1- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Anion exchange; Lipoprotein; Palmitate. DOMAIN 1 392 CYTOPLASMIC (POTENTIAL). DOMAIN 393 918 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
791 POTENTIAL.
817 POTENTIAL.
876 POTENTIAL.
876 POTENTIAL.
876 POTENTIAL.
102223 MW; FF4ECAD6D60CF0CF CRC64;
                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                             Length 922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92344566; PubMed-1637296;
Hubber S., Michel F., Rudloff V., Appelhans H.;
"Amino acid sequence of band-3 protein from rainbow trout
erythrocytes derived from cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                          Score 71; DB 1; Pred. No. 0.00052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 27, Created)
(Rel. 33, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     918 AA.
                                                                                                                                                                                                                                   5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                             01-0CT-1993 (Rel. 27, Created)
01-FFB-1996 (Rel. 33, Last sequ
15-JUL-1999 (Rel. 38, Last and
Band 3 anion exchange protein.
SLC4A1 OR AE1.
                                                                                                                                                                                                                                                                                            1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                          72.48;
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                                                                                                                                                                                                     Local Similarity 66.7 tes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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  774
796
855
653
922 AA;
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PIR; A33638; A33638.
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P23348;
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                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
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                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed-2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                             POTENTIAL.
PALMITATE (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N; 37E163141FEDC16A CRC64;
                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morgans C.W., Kopito R.R.; "Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                                                                Score 63; DB 1; Length 918;
Pred. No. 0.012;
); Mismatches 4; Indels
                       LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- TISSUE SPECIFICITY: NEURONAL.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId-P16283-3; Sequence-VSP_000466, VSP_000467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId-P16283-2; Sequence-VSP_000464, VSP_000465;
  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5. Cell Sci. 106:1275-1282(1993).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-94171936; Pubmed-8126106;
                                                                                                                                                                                                                                                                                  PRT; 1227 AA.
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             POTENTIAL.
EXOPLASMIC
                                                         POTENTIAL. POTENTIAL.
                                  POTENTIAL
                                               POTENTIAL
                                                                                                                               MM;
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                                                                                                                                                                                                                744 SVTHANALTVMSKGPKP 760
                                                                                                                                                                                                  1 SVTHANALTVMGKASTP 17
                                                                                                                                                    64.3%;
76.5%;
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                                                                                                                               101893
                                                                                                                                                                           13; Conservative
                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
                                                                                                                              918 AA;
                                                                                                                                                                Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=14-AE3;
 602
617
638
674
712
772
772
794
853
853
546
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P16283;
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DOMAIN
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                                                                                                                              SEQUENCE
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                                  TRANSMEM
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                                               TRANSMEM
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B3A3_MOUSE
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Massing (in isoform 311-AB3).
/FTId=VSP_000465.
KPLHWPGGDGHRGKSLK -> FCVLRSPSPCLGETVTEGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE—9009439; PubMed—2294114;
MEDLINE—9009439; PubMed—2294114;
Kudrycki K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265.462-471(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- STRSEE SPECIFICITY: NEURONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PALMITATE (BY SIMILARITY).
AALLDLEQTTL -> RAFWAGNESLL (in isoform
                                                                                                     TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                            Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform 14-AE3).
/FTIGH-VSP_000466.
Missing (in isoform 14-AE3).
/FTIGH-VSP_000467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3 OR B3RP3.
                                                                                                                                                                                             CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE)
POTENTIAL.
                                                                                                                                                                                                                                                                                                    POTENTIAL. CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                    POTENTIAL.
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HSSP; P02730; 1BTQ.
MGD; MGI:109350; S1C443.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1048 SVTHVNALTVMRTAIAPG 1065
                                                              Pfam; PF00955; HC03_cotransp; 1. PRINTS; PR01231; HC03TRNSPORT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1227 AA; 135164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.2%;
Best Local Similarity 72.2%;
Matches 13; Conservative
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                                                                                                                                                                                                                                                                 815
846
905
920
941
997
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868
1160
391
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   between the Swiss institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain band 3-like protein) (CAE3/BAE3).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                        InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
InterPro; IPR003020; HCO3_cotranspt.
PRIM: PR00251; HCO3_TRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
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TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIGR00834; ae; 1.
TIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1227;
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POLY-LEU.
WW: 3EB1620EE011730E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                        MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.034;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
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MEDLINE-95008042; PubMed-7923606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SVTHANALTVMGKASTPG 18
                                                                                                                                                                                                                                                                                                                            Lipoprotein;
707
                                                                                                                                          EMBL; J05167; AAA40798.1; -. PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.2%;
72.2%;
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1227 AA; 135406
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Best Local Similarity 72.2
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1160
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997
                                                                                                                                                                               HSSP; P02730; 1BTQ
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P48751;
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                                                                                                                                                                                                                                                                                                   EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=P48751-2; Sequence-VSP_000462, VSP_000463;
-!- TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING VENTRICLE.
                                                                                                                                                TISSUE-Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: PLASMA MEMBRANE ANTON EXCHANGE PROFEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(?)/HCO3(.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PFUUJU; HC03TKWJ. ...
PRINTS; PRO1211; HC03TKWJ. as; 1.
TIGREMMs; TIGRO0834; ae; 1.
PRO5ITE; PS00219; ANION_EXCHANGER_1; 1.
PRO5ITE; PS00220; ANION_EXCHANGER_2; 1.
PRO5ITE; PS00220; ANION_EXCHANGER_2; 1.
PRO5ITE; PS00220; ANION_EXCHANGER_2; 1.
PRO5ITE; PS00220; ANION_EXCHANGER_2; Alternative splicing.
"Molecular cloning, expression, and chromosomal localization of isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005452; F:inorganic anion exchanger activity; TAS.
GO; GO:0006832; P:small molecule transport; TAS.
InterPro; IPR001117; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
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Missing (in isoform CAE3)
/FTId-VSP_000462.
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                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Integral membrane protein -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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                                                                                                                        SEQUENCE FROM N.A. (ISOFORM CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U05596; AAA50748.1; -.
EMBL; L27213; AAB05850.1; -.
PIR; I38496; I38496.
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Genew; HGNC:11029; SLC4A3.
MIM; 106195; -.
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1002
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11128
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11165
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POTENTIAL. POTENTIAL.
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72.2%;
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                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
                                                                                                                                                                                                                                                                                          446
1188
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1003
1050
1129
1192
874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
Y003_HAEIN
ID Y003_HAEIN
                                                                                                          TRANSMEM
                 TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
Pfam; PF00955; HC03_cotranspt.
TIGRRAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transmembrane; Glycoprotein; Transmembrane; Liproprotein; Palmitate.
DOMAIN : 1.709
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
                                                                                                                                                                                                                                                                                                                           Score 61; DB 1; Length 1232;
Pred. No. 0.034;
0; Mismatches 5; Indels
                                                                                                                                                                                           S -> C (IN REF. 2).
S -> G (IN REF. 2).
R -> E (IN REF. 2).
L -> P (IN REF. 2).
M. -- B (IN REF. 2).
M. -- B (IN REF. 2).
W. -- B (IN REF. 2).
W. -- B (IN REF. 2).
 SPS -> MPA (in isoform CAE3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Kidney;
Abuladze N., Pushkin A., Kurtz I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: FLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMBRANE (ANION EXCHANGE) POTENTIAL.
             /FTIG=VSP_000463.

I -> V (IN REF. 2).
P -> S (IN REF. 2).
S -> G (IN REF. 2).
S -> G (IN REF. 2).
GS -> F (IN REF. 2).
F -> L (IN REF. 2).
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A -> S (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
B -> S (IN REF. 2).
C -> D (IN REF. 2).
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-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                          1232 AA; 135706 MW;
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                                                                                                                                                                                                                                                                                                                             62.2%;
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nes 13; Conservative
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MEDLINE-2013/488; Pubmed-10675023;
Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
Gray C., Fountoulakis M.;
"Two-dimensional map of the proteome of Haemophilus influenzae.";
Electrophoresis 21:411-429(2000).
-1- SIMILARITY: BELONGS TO THE COF/TBHA/YIDA/YIGL (E.COLI) / YCSE/YXEH·
(B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 61; DB 1; Length 1233; Pred. No. 0.034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE486423E9818583 CRC64;
POTENTIAL. CYTOPLASMIC (POTENTIAL).
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01-NoV-1995 (Rel. 32, Last sequence update)
228-FEB-2003 (Rel. 41, Last annotation update)
Protein HI0003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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0;
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 49; DB 1; Length 262; Best Local Similarity 55.6%; Pred. No. 0.73; Matches 10; Conservative 4; Mismatches 4; Indels
                                                                                        InterPro; IPR006379; HAD_SF_IIB.
InterPro; IPR006834; Hydrolase.
InterPro; IPR0010150; Hypothet_cof.
Pfam; PF00702; Hydrolase; 1.
TIGRFAMS; TIGR00099; Cof-subfamily; 1.
TIGRFAMS; TIGR01484; HAD-SF-IIB; 1.
PROSITE; PS01228; CoF_1; 1.
Complete profecome.
SEQUENCE 262 AA; 29353 MW; 2E9657AC4F2093DC CRC64;
                                                                                                                                                                                                                                                                                                                                                   3 THANALTVMGKASTPGAA 20
                                          EMBL; U32686; AAC21682.1; -. PIR; 164139; 164139. TIGR; H10003; -.
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Search completed: September 3, 2003, 11:46:56 Job time : 10.25 secs

qq

us-10-087-464-3.rsp

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2003, 11:25:42; Search time 9.25 Seconds
(without alignments)
101.679 Million cell updates/sec Run on:

US-10-087-464-3 96 1 GRASTPGAAAQIQEVKEQRI 20

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1	P23562 rattus norv	P04919 mus musculu	P15575 gallus gall	rattus	P13808 mus musculu	P48746 oryctolagus	Q9z0s8 cavia porce		P16283 mus musculu	P23348 rattus norv		_		_		Q63083 rattus norv			P38055 escherichia		P53890 saccharomyc	P16252 haemonchus	٠.	-	_	Q81999 human papil		Q62468 mus musculu	Q9x764 lactococcus	P08799 dictyosteli	<u>ი</u>	P30848 escherichia
SUMMARIES	DI	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_CAVPO	B3A2_HUMAN	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	RRPP_MUMPE	RRPP_MUMPM	NCB1_MOUSE	NCB1_RAT	NCB1_HUMAN	RLOC_ARATH	YDJE_ECOLI	CORO_SCHPO	YNQ6_YEAST	CAC2_HAECO	BASP_RAT	DH47_ARATH	FOJO_DROME	VE1_HPV72		VIL1_MOUSE	IF2_LACLC		SPCA_HUMAN	PROP_ECOLI
	Query Match Length DB	911		929 1	922 1	1234 1	1237 1	1237 1	1238 1	1241 1	1227 1	1227 1	1232 1	1233 1	391 1	391 1	459 1	459 1	461 1	323 1	452 1	601 1	448 1	210 1	219 1	265 1	583 1	650 1	826 1	826 1	950 1	2116 1	2418 1	500 1
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PROP_SALTY PKP1 MOUSE	RL7_ANASP HAP3_YEAST	RK12_TOBAC	PRS4_ORYSA	RADA_CHLPN	ATPA_MYCPN	. CIK1_YEAST	UL93_HCMVA
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3.4 3.5	36	38	40	41	43	44	45

ALIGNMENTS

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PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904.
MEDLINE=20400020; PubMed=10942405;
Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono E.,
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Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
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Okubo K., Hamasaki N., Hara K., Kageura M.;
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Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
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Submitted (XXX-1992) to the EMBL/Genbank/DDBJ databases.
Submitted (XXX-1992) to the EMBL/Genbank/DDBJ databases.

-!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CXTODALASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSRELETAL AND OTHER PROTEINS (BY SIMILARITY)
-!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
SLC4A1 OR AEI.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
     Length 911;
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                                                     Indels
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100.0%; Score 96; DB 1; I
ilarity 100.0%; Pred. No. 2.6e-07;
Conservative 0; Mismatches 0;
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IsoId=P23562-2; Sequence=VSP_000455;
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IsoId=P23562-1; Sequence=Displayed;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
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                                                                                                  TISSUE=Kidney;
MEDLINE=89255254; Pubmed=2722777;
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                                                                                                                                                                                                                                                                                    STANDARD;
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Best Local Similarity
Matches 20; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
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13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITATE (BY SIMILARITY).
MISSING (In Isoform Kidney).
/FIIG-VSP.000455.
% 681A228474E5E9DE CRC64;
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Kopito, R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL)
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               CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
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MEDLINE-86034211; PubMed-3840489;
Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 89; DB 1; I
Pred. No. 3.4e-06;
0; Mismatches 1;
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MEDLINE-85268011; PubMed-2410791;
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95.08;
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Nature 316:234-238(1985).
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Best Local Similarity
Matches 19; Conserv
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SLC4A1 OR AE1
 Lipoprotein;
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LIPID
VARSPLIC
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B3AT_CHICK
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                                                                                                                                                                       HEMOGLOBIN.
SUBUNT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                           Major proteolytic fragments of the murine band 3 protein as obtained
                                                                                                                            Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: ERYTHROCYTE.
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (PROBABLE).
                                                                                                                                                                                                                                                                 SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSOU220; ANION_EXCHANGER_1; 1.
PROSITE; PSOU220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 423 929 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL) POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                         Event-Alternative splicing; Named isoforms=2;
                                                                                            SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed=2713407;
                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId-P04919-2; Sequence-VSP_000454;
                                                                                                                                                                                                                                                                                                                                                                         Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
POTENTIAL.
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HGO3_cotranspt.
PR00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORT.
TIGRRAMs; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X02677; CAA26506.1; -. EMBL; M29379; AAA37187.1; -. EMBL; J02756; AAA37278.1; -. EMBL; X03917; CAA27555.1; -. PIR; A25314; A25314;
                                                 band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P02730; 1BTS
                                                                                                                                                                                                                                                                                                                                                                                                       Name-Kidney;
                                                                                                                                              Passow H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-89039870; PubMed=318555;
MEDLINE-89039870; PubMed=318555;
MEDLINE-89039870; PubMed=318555;
Win H. R.C., Yaw N.S., Ansorge W., Voss H., Schwager C.,
Vennstroem B., Zenke M., Engel J.D.;
"Two different mRNAs are transcribed from a single genomic locus encoding the chicken erythrocyte anion transport proteins (band 3).";
Mol. Cell. Biol. 8:4416-4424(1988).
INTEGRAL DOMAIN BAND 3 IS THE MAJOR INTEGRAL GLYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN WHEREAS ITS CYTODALSMIC DOMAIN PROVIDES BINDING SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBDITT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-FBB-1996 (Rel. 13, Last annotation update)
Band 3 anion transport protein.
Gallus gallus (Chicken).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                           Gaps
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                          79 Missing (in isoform Kidney).

7/FIGA'VSP_000454.

467 G -> S (IN REF. 5).

103135 MW; 5C0E281C394FB614 CRC64;
     PALMITATE (BY SIMILARITY)
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                                                                                                                                                       92.7%; Score 89; DB 1; 1
95.0%; Pred. No. 3.4e-06;
                                                                                                                                                                                                         0; Mismatches
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR001302; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                       1 GKASTPGAAAQIQEVKEQRI 20
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                                                                                                                                                                               Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
861
79
                                                                                 467
                                                                                                     929 AA;
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IsoId=P13808-1; Sequence=Displayed
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   SO SET THE FETT THE F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kudryck1 K.E., Newman P.R., Shull G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that
are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kopito R.R.; "Functional expression and subcellular localization of an anion
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (PROBABLE); FF4ECAD6D6OCFOCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exchanger cloned from choroid plexus.";
Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                                                                                                                                             Score 61; DB 1; Length 922,
 EXOPLASMIC LOOP (POTENTIAL)
                                   CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                    5; Indels
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-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                   Pred. No. 0.087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1234 AA.
                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                                                                        POTENTIAL.
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InterPro: IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PRINTS: PR01231; HCO3TRNSPORT.
TIGRPAMS; TIGR00834; ae; 1.
                                                                                                                                                                                                                                                                                                                                                753 GKSAVPGERAHIVEVKEQRL 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Stomach;
MEDLINE-90094439; PubMed=2294114;
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                                                                                                                                                                                                                                                                                                                          1 GKASTPGAAAQIQEVKEQRI 20
                                                                                                                                                                                                             102223 MW;
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                                                                                                                                                                                                                                                                                    12; Conservative
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Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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DOMAIN
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                                                     FRANSMEM
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Gaps
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P13808; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
84-FCB-2003 (Rel. 41, Last annotation update)
84-CAA2 OR AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-89034212; PubMed-3182834;
Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
"Cloning and characterization of a murine band 3-related cDNA from kidney and from a Lymphold cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY. MEDLINE-20462926; PubMed-11006093; Lecanda J., Urtasun R., Medina J.F.; "Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exchanger gene.";
Biochem. Biophys. Res. Commun. 276:117-124(2000).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 58; DB 1; Length 1234;
Pred. No. 0.35;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALMITATE (BY SIMILARITY).

G -> A (IN REF. 2).

RR -> PG (IN REF. 2).

M -> I (IN REF. 2).

M -> I (IN REF. 2).

M -> I (IN REF. 2).

M -> I (IN REF. 2).
                                                                                                                                                                           POTENTIAL.
POTENTIAL.
EXOPLASMIC LOOP (POTENTIAL).
                                                                                         CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                             POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC
                                                                                                                                                      POTENTIAL.
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Conservative
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Matches 12; Conserv
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B3A2_RABIT
                                     CONFLICT
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                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                            TISSUE SPECIFICITY: ISOform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; AJLING, 1BTU.

R MGD; MGI:109351; S1c4a2.

R MGD; MGI:109351; S1c4a2.

R InterPro; IPR001771; Anion_exchange.

DR InterPro; IPR003020; HCO3_cotranspt.

DR PRIME; PR00955; HCO3_cotranspt.

DR PRIME; PR001231; HCO3TRNSPRT.

DR PROSITE; PS00220; ANION_EXCHANGER_1; 1.

DR PROSITE; PS00220; ANION_EXCHANGER_2; 1.

R MG Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

R M Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;

Anion exchange; Lipoprotein; Panilates, Alternative splicing.

CYTOPLASMIC (POTENTIAL).

MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform C1).
/FTId=VSP_000460.
ERTSPSPPTQTPHQEAAPRASKGAQTG -> MPAFQEWKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALMITATE (BY SIMILARITY).
MSSAPRRPASGADSLHT -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSAPRRPASGADSLHT -> MTQ (in isoform B1)
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                              IsoId=P13808-5; Sequence=VSP_000459, VSP_000461;
                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
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3P_000459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /FTId=VSP_000457.
                                                     IsoId=P13808-3; Sequence=VSP_000457;
                 IsoId=P13808-2; Sequence=VSP_000458;
                                                                                           IsoId=P13808-4; Sequence=VSP_000460;
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HIS-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF255774; AGG23154.1; ...
EMBL, AF255774; AGG23155.1; ...
EMBL, AF255774; AGG23156.1; ...
EMBL, AF255774; AGG23158.1; ...
EMBL, AF255774; AGG23158.1; ...
PIR; A31789; A31789.
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                                                                                                                                                                              ö
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=New Zealand white;
MEDILINE=93035730; PubMed=1415547;
Chow A., Dobbins J.W. Tronson P.S., Igarashi P.;
"CDNA cloning and localization of a band 3-related protein from
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Am. J. Physiol. 263:G345-G352(1992).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION.
                                                                                                                         Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -, 1.
-,ycoprotein; Transport; Antiport; Ion t
e; Lipoprotein; Palmitate.
1 703 CYTOPLASMIC (POTENTIAL).
4 127 MEMBRANE (ANION EXCHANGE).
727 POTENTIAL.
770 POTENTIAL.
813 POTENTIAL.
843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                            Indels
                        /FTId=vSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                         DB 1;
                                                                                                                                                 Pred. No. 0.35;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. POTENTIAL.
                                                                                                                         Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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PIR; A56764; A56764.
HSSP; P02730; IBTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR03920; HCO3_cotranspt.
                                                                                                                                                                                                                                                          1069 KAVAPGDKPKIQEVKEQRV 1087
                                                205 A -
136813 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                               2 KASTPGAAQIQEVKEQRI 20
                                                                                                                         60.4%;
                                                                                                                                                 Local Similarity 63.2
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                205 20
1237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anion exchange;
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POTENTIAL

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931
985
1033
1088
1160
                                                                                          865
879
1170
1238
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                                                                                                                                                                                                                                                                         B3A2_HUMAN
                                                                              CARBOHYD
CARBOHYD
              TRANSMEM
TRANSMEM
                                                                                                     CARBOHYD
                                                                                                                            SEQUENCE
   TRANSMEM
                                 TRANSMEM
                                              TRANSMEN
                                                        DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-NIH 2; TISSUE-Organ of Corti;
MEDLINE-32787; PubMed-9804866;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
Mhatre A.N., Charachon G., Alper A.L., Lalwani A.K.;
"The guinea pig cochlear AE2 anion exchanger: cDNA cloning and in situ localization within the cochlea.";
Biochim. Blophys. Acta 1414:1-15(198).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                            Gaps
                                                                                                                                                                                                                                          28 -C1-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2 anion exchanger).
                                                                                                                                                                                                                                                                                                                 Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITAE (BY SIMILARITY).
W; 2811D11051552BB2 CRC64;
                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                           ő
                                                                                                   DB 1; Length 1237;
                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXOPLASMIC LOOP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anion exchange; Lipoprotein; Palmitate.
DOMAIN 1 704 CYTOPLASMIC (POTENTIAL).
DOMAIN 705 1238 MEMBENNE (ANION EXCHANGE)
TRANSMEM 705 728 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
                                                                                                    Score 58; DB 1;
Pred. No. 0.35;
                                                                                                                                                                                                                            PRT; 1238 AA
                                                                                                                           Mismatches
           PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
                   74 88 HIS-R
85 855 N-LIN
864 864 N-LIN
878 878 N-LIN
1169 1169 PALMI
1237 AA; 136535 MW; D
                                                                                                                                                           1069 KAVAPGDKPKIQEVKEQRV 1087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                        2;
                                                                                                                                              2 KASTPGAAQIQEVKEQRI 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF121253; AAD19700.1; -. HSSP; P02730; 1BTQ.
                                                                                                   60.4%;
63.2%;
                                                                                                                            Conservative
                                                                                                                                                                                                                            STANDARD;
                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISTRIBUTION
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734
734
731
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898
916
                                                                                                                       12;
                                                                                                                                                                                                                           B3A2_CAVPO
Q9Z0S8;
                                CARBOHYD
CARBOHYD
CARBOHYD
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DOMAIN
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Best Local
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                                                                  LIPID
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                                                                                                                         Matches
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RC TISSUE—Brain;

RX MEDLINE—22388257; PubMed—12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halseh F.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Prange C.,

RA Brownstehn M.J., Godin T.B., Toshlywik S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Schergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Human and mouse CDNA sequences.";

R Human and mouse CDNA sequences.";

R Human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P04920; 0969L3;
13-AUG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AEZ OR EFB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86274622; PubMed-3015590; Demuth D.R., Showe L.C., Ballantine M., Palumbo.A., Fraser P.J., Cioe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid band 3-like protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                         65 N-LINKED (GLCNAC. . .) (POTENTIAL).
79 N-LINKED (GLCNAC. . .) (POTENTIAL).
70 PALMITATE (BY SIMILARITY).
137358 MW; FA1739862ED5ADBF CRC64;
                                                                                                                                                     PRO-RICH.
HIS-RICH.
N-LINEAD (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                  Score 58; DB 1
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1241 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1130:326-328(1992).
                                                        POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KASTPGAAAQIQEVKEQRI 20
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                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 63.2%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
951
1007
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1133
1196
316
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Name=FL-AE3
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   CONFLICT
                     CONFLICT
                                       SEQUENCE
                                                           Query Match
                              CONFLICT
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B3A3_MOUSE
                                                                              Matches
                                                                                                                                                                     FFFFS
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                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLGHHHGQGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PALMITATE (BY SIMILARITY).
MSSAPRLPAKGADSFCT -> MTQ (in isoform
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport;
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 1 708 1241 MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-RICH.

LLIKKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
EMBO J. 5:1205-1214(1986).
-1- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTPTSPSLSWEVFLR (IN REF. 3).
EL -> DV (IN REF. 1 AND 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXOPLASMIC LOOP (POTENTIAL)
                                                                                              Isold-P04920-2; Sequence-VSP_000456;
SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                           SUBCELLUIAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E -> M (IN REF. 1).
H -> R (IN REF. 1).
D -> G (IN REF. 1).
E -> V (IN REF. 1).
Q -> R (IN REF. 1).
E -> R (IN REF. 1).
MISSING (IN REF. 1).
L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                               MIM 109280; -.

GO; GO:0005624; C:membrane fraction; TAS.

GO; GO:0005629; F:anion transporter activity; TAS.

GO; GO:0006810; F:anion transport; TAS.

InterPro; IPR0031717; Anion_exchange.

InterPro; IPR003020; HCO3_cotranspt.

PRAINTS: PR01231; HCO3TRNSPORT.

IIGRFAMS; TIGR00834; ae: 1.
                                                Event=Alternative splicing; Named isoforms=2; Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP_000456
                                                                           IsoId=P04920-1; Sequence=Displayed;
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EMBL; BC009386; AAH09386.1; -.
EMBL; BC009434, AAH09434.1; -.
EMBL; X03918; CAA27556.1; -.
PIR; S21086; S21086.
HSSP, PO2730, IBTQ.
Genew; HGNC:11028; SLC4A2.
MIM; 109280; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   933
954
1010
1059
11136
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320
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1163
                                                                                       Name=B1;
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DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                          Gaps
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-90075236; Pubmed-2686841;
Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-9471936; PubMed-8126106;
Morgans C.W., Kopito R.R.;
Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                                                                                        DB 1; Length 1241;
                         REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-006-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P16283-3; Sequence=VSP_000466, VSP_000467;
- TISSUE SPECIFICITY: NEURONAL.
- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F. Cell Sci. 106:1275-1282(1993).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                        No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1227 AA.
                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P16283-1; Sequence=Displayed;
                                                                                                                                                                            Score 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A33638; A33638.
HSSP, POY230; LBTQ.
MGD; MGT:109350; Slc4a3.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PP00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3_TRNSPORT.
                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                        1073 KAVAPGDKPKIQEVKEQRV 1091
                                                                                                                                                                                                                                                                                               2 KASTPGAAAQIQEVKEQRI 20
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                                                        824 824
902 902
1241 AA; 136966
                                                                                                                                                                            60.48;
                                                                                                                                                                                                           63.2%;
                                                                                                                                                                                                     Best Local Similarity 63.2 Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=311-AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=14-AE3;
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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular cloning, expression, and chromosomal localization of two isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              InterPro; IPR01117; Anion_exchange.
InterPro; IPR010120; HCO3_cotranspt.
InterPro; IPR00120; HCO3_cotranspt.
PRIMIS; PR01231; HCO3_ENTERSPORT.
IGREAMS; TIGR00834; ae; 1.
FROSITE; PS002219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Heart;
MEDLINE-95008042; PubMed-7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1227;
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PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                 MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 1;
Pred. No. 1.5;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1232 AA.
                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                 POTENTIAL. POTENTIAL.
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POTENTIAL.
POTENTIAL.
     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
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POLY-PRO.
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POLY-LEU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anion exchange protein 3 (Neuron
band 3-like protein) (CAE3/BAE3)
SLC4A3 OR AE3.
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nilarity 61.1%;
Conservative 2
                                  EMBL; J05167; AAA40798.1; -. PIR; B34911; B34911.
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es 11; Conserv
                                                                    P02730; 1BTO
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P48751;
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                                                                                                                                                                                                                                                                                                                                                                          /FTIG=VSP_000464.
Missing (in isoform 311-AE3).
/FTIG=VSP_000465.
KPLHMPGGDGHRGKSLK -> FCVLRSPSPCLGETVTEGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
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/FTId=VSP_000467.
W; D5BEC46E03F4251C CRC64;
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28-FBB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AB3 OR B3RP3.
                                                                                CYTOPLASMIC.
MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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PALMITATE (BY SIMILARITY
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61.1%;
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                     ISOId=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE.SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Transport; Antiport; Ion transport; Infoprotein; Palmitate; Alternative splicing. 1708 CYTOPLASMIC. 2710PLASMIC. MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                      MIM; 106195; -

4 GO; GO:0005624; C::integral to plasma membrane; TAS. .

5 GO; GO:0005624; C::membrane fraction; TAS. .

5 GO; GO:0005452; F::inorganic anion exchanger activity; TAS. .

5 GO; GO:0006832; P::anall molecule transport; TAS. .

8 InterPro; IPR001717; Anion_exchange.

8 InterPro; IPR001717; Anion_exchange.

8 PRIMF; PR00955; HCO3_cotranspt. .

8 PRIMF; PR00955; HCO3_cotranspt. .

8 PRIMF; PR001231; HCO3_TRNSPORT. .

8 PROSITE; PS00219; ANION_EXCHANGER_1; 1.

8 PROSITE; PS00219; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform CAE3).
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                                                                                                                                                  SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                      CL(-).
SUBCELLULAR LOCATION: Integral membrane protein.
                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                              Comment=Additional isoforms seem to exist;
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                                                                                                IsoId=P48751-1; Sequence=Displayed;
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EMBL, L27213; AAB05850.1; --
PIR, I38496; I38496.
HSSP, P02730; 1BTQ.
Genew; HGNC:11029; SLC4A3.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein; 1708 (1232 N) (1232 N)
                                                           ALTERNATIVE PRODUCTS
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Anion exchange;
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466
608
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                                                                                       Name-BAE3;
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                                                                                                            Name=CAE3
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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PRINTS; PR01231; HCO3TRNSPORT.
PRINTS; PR01231; HCO3TRNSPORT.
PROSTE; PS00219; ANION_EXCHANGER_1; 1.
PROSTE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
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30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó;
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1232;
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1825BE15977C3821 CRC64;
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Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
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-!- TISSUE SPECIFICITY: NEURONAL.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
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                                                                                                             (IN REF. 2)
       -> FI (IN REF. 2)
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2; Mismatches
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
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Best Local Similarity 61.1
Matches 11, Conservative
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1232 AA;
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Search completed: September 3, 2003, 11:46:57 Job time: 10.25 secs
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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Takeuchi K., Hishiyama M., Yamada A., Sugiura A.;
Takeuchi K., Hishiyama M., Yamada A., Sugiura A.;
"Molecular cloning and sequence analysis of the mumps virus gene encoding the P protein: mumps virus P gene is monocistronic.";
J. Gen. Virol. 69:2043-2049(1988)
-!-FUNCTION: THIS PROPEIN IS PROBABLY A COMPONENT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                   N-LINKED (GLCNAC. . .) (POTENTIAL). PALMITATE (BY SIMILARITY).
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01-APR-1990 (Rel. 14, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
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                                                                                                                                   AE486423E9818583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Mumps virus (strain Enders).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11167;
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Transferase; RNA-directed RNA polymerase; Nucleocapsid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 AA; 41650 MW; 2802A11A5542B7A5 CRC64;
                                                                                                                                                          DB 1;
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POLY-LYS.
POLY-SER.
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Conservative
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Matches 10; Conservative
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"Molecular Clohing and Sequence analysis of the mumps virus gene
encoding the P protein: mumps virus P gene is monocistronic.";
J. Gen. Virol. 69:2043-2049(1988).
--- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
POLYMERASE. IT MAY FUNCTION IN TEMPLATE BINDING.
--- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
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                                                         01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
RNA polymerase alpha subunit (EC 2.7.7.48) (Nucleocapsid
                                                                                                                                                                                                                                              Mumps virus (strain Miyahara vaccine).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Rubulavirus.
NCBI_TaxID=11171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004897; Paramyx_P_V.
Pfam; PF03210; Paramyx_P_V; 1.
Transferase; RNA-directed RNA polymerase; Nucleocapsid;
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391 AA.
   PRT;
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MEDLINE-88299965; PubMed-3404121;
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153 KRGGPGAAQGQTIQEEGI 171
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Matches
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

September 3, 2003, 11:25:42 ; Search time 9.25 Seconds
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101.679 Million cell updates/sec Run on:

US-10-087-464-4 112 1 DRILLLEKPPKYHPDVPYVK 20 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		rattu	P04919 mus musculu	5575 gallus gall	rattus		_			P16283 mus musculu			018917 oryctolagus		homo	-					7764 mus musculu	_		Q64903 african hor		4905 african hor	uj83 homo sapien					8509	9712 anabaena sp
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SUMMARIES	ID	B3AT_HUMAN	B3AT_RAT	B3AT_MOUSE	B3AT_CHICK	B3A2_RAT	B3A2_MOUSE	B3A2_RABIT	B3A2_HUMAN	B3A2_CAVPO	B3A3_MOUSE	B3A3_RAT	B3A3_HUMAN	B3A3_RABIT	SOC7_HUMAN	LEGC_HUMAN	SOC7_MOUSE	B3AT_ONCMY	UL16_EBV	PPAF_ARATH	SIA1_MOUSE	WBP1_MOUSE	CYNS_ORYSA	YB46_METTH	VNS3_AHSV1	VNS3_AHSV2	VNS3_AHSV8	HPCL_HUMAN	SIA1_RAT	SIA1_HUMAN	NO75_LUPLU	DNLI_THEVO	DM3B_MOUSE	Y458_ANASP
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de	Query Match	100.0	96.4	96.4	73.2	66.1	66.1	66.1	66.1	65.2	60.7	60.7	55.4	55.4	51.8	46.4	44.6	44.6	43.8	43.8	42.9	42.4	42.0	42.0	41.1	41.1	41.1	41.1	40.2	0	0	40.2	40.2	39.3
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Q58094 methanococc	Q00024 agaricus bi	P70711 rattus norv	P21734 saccharomyc	Q00341 homo sapien	P81021 gallus gall	Q01197 gossypium h	P06503 trichoplusi	O12705 xestia c-ni	P38552 rattus norv	P50108 saccharomyc	Q9uqq2 homo sapien
TKTN_METJA	PPO1_AGABI	UB5D_RAT	UBC1_YEAST	VGLN_HUMAN	VGLN_CHICK	E6_GOSHI	GRAN_GVTN	GRAN_GVXN	LEG4_RAT	MN10_YEAST	LNK_HUMAN
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274	268	147	215	1268	1270	238	248	248	324	393	575
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44	44	43.5	43.5	43.5	43.5	43	43	43	43	43	43
34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1	1.1.1
	ID	DOST_HUMAN STANDARD; PRT; 911 AA.
	S F	(Rel.
	占占	01-APR-1990 (Rel. 14, Last sequence update) 15-SRP-2003 (Rel. 42, Last annotation undate)
	DE	Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
	G DE	(CD233 antigen). SLC4Al OR AE1 OR EPB3 OR DI.
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	88	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia: Euthoria: Drimatos: Catarrhini: Hominidae: Homo
	38	bucilet 14, filmaces,
	RN G	[1]
	Z Z	SEQUENCE FROM N.A. MEDLINE=90083213; PubMed=2594752;
	RA	Lux S.E., John K.M., Kopito R.R., Lodish H.F.;
	X 0	"Cloning and characterization of pand 3, the human erythrocyte anion: exchange protein (1811) ".
	R.L	Proc. Natl. Acad. Sci. U.S.A. 86:9089-9093(1989).
	RN	[2]
	7 Z	JISSUENCE FROM N.A.
	RX	MEDLINE=89134172; PubMed=3223947;
	RA	S.;
	χ Ε	"The complete amino acid sequence of the numan erythrocyte membrane
	Z. Z.	ב
	RN	
	RP X	SEQUENCE OF 1-199; 220-292 AND 347-370. MEDITNE=90001294: PubMed=2790053:
	RA	Yannoukakos D., Vasseur C., Blouguit Y., Bursaux E., Wajcman H.;
	RŢ	"Primary structure of the cytoplasmic domain of human erythrocyte
	R i	protein band 3. Comparison with its sequence in the mouse.";
	Z Z	biodiiiii. biopiiys. Acca 930:43-49(1309). [4]
	RP.	SEQUENCE OF 1-201.
	X Z	MEDLINE=83238395; PubMed=6345535; Kani R K Murthv S N D Reddv A G Steck T I Kohler H .
	R	"Amino acid sequence of the N alpha-terminal 201 residues of human
	E i	erythrocyte membrane band 3.";
	7 Z	J. BIOI. CNem. 258:/981-/990(1983).
	Z dz	SEQUENCE OF 1-3.
	RX	MEDLINE=79027186; PubMed=701248;
	RA E	Drickamer L.K.;
	Z 52	Torrencation of the band 3 polypeptide from numban erythrocyce membranes. Identification of NH2-terminal sequence and site of
	RT	carbohydrate attachment.";
	RL PN	J. Blol. Chem. 253:/242-/248(1978).
	R P	(8) SEQUENCE OF 559-630.
	X.	MEDLINE-83308584; Pubmed-6615451;
	RA E	Brock C.J., Tanner M.J.A., Kempf C.;
_	2	"ine numan erytniocyte anion-transport protein. Partial amino acid

Pinna L.A., Donella-Deana A.;
"Sequential phosphorylation of protein band 3 by Syk and Lyn tyrosine kinases in intact human erythrocytes: identification of primary and secondary phosphorylation sites.";
Blood 96:1550-1557(2000). Hamasaki N.; VARIANT MEMPHIS GLU-56.
MEDLINE-91329825; Pubmed-1678289;
Yannoukakos D., Vasseur C., Driancourt C., Blouquit Y., Delauney J.,
Wajcman H., Bursaux E.,
"Human erythrocyte band 3 polymorphism (band 3 Memphis):
characterization of the structural modification (Lys 56-->Glu) by
Blood 78:1117-1120(1991). VARIANT HE 400-ALA--ALA-408 DEL, AND VARIANT MEMPHIS GLU-56. MEDLINE=92107882; PubMed=1722314;
Jarolim P., Palek J., Amato D., Hassan K., Sapak P., Nurse G.T.,
Rubin H.L., Zhai S., Sahr K.E., Liu S.-C.;
"Deletion in erythrocyte band 3 gene in malaria-resistant Southeast Asian ovalocytosis."; conformation and a possible molecular mechanism for anion PHOSPHORYLATION OF TYR-8; TYR-21; TYR-359 AND TYR-904. MEDLINE-20400020; PubMed-10942405; Brunati A.M., Bordin L., Clari G., James P., Quadroni M., Baritono SEQUENCE OF 834-911.
MEDLINE-88228050; PubMed-3372523;
Kawano Y., Okubo K., Tokunaga F., Miyata T., Iwanaga S., Hamasaki
"Localization of the pyridoxal phosphate binding site at the COOHterminal region of erythrocyte band 3 protein.";
J. Biol. Chem. 263:8232-8238(1988). Jennings M.L., Smith J.S.; "Anion-proton cotransport through the human red blood cell band 3 protein. Role of glutamate 681."; J. Biol. Chem. 267:13964-13971(1992). "Band 3 Tuscaloosa: Pro-327-->Arg substitution in the cytoplasmic domain of erythrocyte band 3 protein associated with spherocytic hemolytic anemia and partial deficiency of protein 4.2."; Blood 80:523-529(1992). VARIANT HE 400-ALA--ALA-408 DEL.
MDELINE-2167271; PubMed-1538405;
SChoffeld A.E., Tanner M.J.A., Pinder J.C., Clough B., Bayley P.M. Nash G.B., Dluzewski A.R., Reardon D.M., Cox T.M., Wilson R.J.M., Okubo K., Hamasaki N., Hara K., Kageura M.;
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"Human erythrocyte protein 4.2 deficiency associated with hemolytic anemia and a homozygous 40 glutamic acid-->lysine substitution in the cytoplasmic domain of band 3 (band 3Montefiore).";
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                                                                                                                                                                                                                                                                                                                  VARIANT BLOOD GROUP DI(A)/MEMPHIS-II.
MEDLINE-94266802; PubMed-8206915;
MEDLINE-94266802; PubMed-8206915;
"Baruce L.J., Anstee D.J., Spring F.A., Tanner M.J.;
"Band 3 Memphis variant II. Altered stilbene disulfonate binding and the Disgo (Dia) blood group antigen are associated with the human exythrocyte band 3 mutatlon Pro-884-->Leu.";
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MEDLINE=96136073; PubMed=8547122;
Maillet P., Vallier A., Reinhart W.H., Wyss E.J., Ott P., Texier P.,
Baklouti F., Tanner M.J., Delaunay J., Alloisio N.;
"Band 3 Chur: a variant associated with band 3-deficient hereditary spherocytosis and substitution in a highly conserved position of
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Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Ebornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;
"Ankyrin-1 mutations are a major cause of dominant and recessive hereditary spherocytosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS HS SER-147 AND MET-488.
MEDLINE=97351102; PubMed=9207478;
Alloisio N., Texier P., Vallier A., Ribeiro M.L., Morle L., Bozor
Bursaux E., Maillet P., Goncalves P., Tanner M.J., Tamagnini G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Changes in the blood group Wright antigens are associated with mutation at amino acid 658 in human erythrocyte band 3: a site cinteraction between band 3 and glycophorin A under certain conditions.";
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MEDLINE=95134893; PubMed=7530501;
Jarolim P., Rubin H.L., Brabec V., Chrobak L., Zolotarev A.S.,
Alper S.L., Brugnara C., Wichterle H., Palek J.;
"Mutations of conserved arginines in the membrane domain of err
band 3 lead to a decrease in membrane-associated band 3 and to
phenotype of hereditary spherocytosis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruce L.J., Ring S.M., Anstee D.J., Reid M.E., Wilkinson S.,
                                                                                                                                             MEDLINE-93229758; Pubmed-8471774;
Rybicki A.C., Qiu J.J.H., Musto S., Rosen N.L., Nagel R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS HS ASP-285; GLU-455; PRO-707; PRO-834 AND MET-837.
MEDLINE-97099297; Pubmed-8943874;
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MEDLINE-95111140; Pubmed-7812009;
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Br. J. Haematol. 91:804-810(1995)
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                                                                                                                              VARIANT MONTEFIORE LYS-40
                                                                                                                                                                                                                                                                             Blood 81:2155-2165(1993).
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                                                                                                                                                                                           Schwartz R.S.;
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VARIANTS HS
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                                                                                                                                                                                                                                                                                                                                                                                                                 Kudrycki K.E., Shull G.E.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: BAND 3 HAS TWO FUNCTIONAL DOMAINS: ITS INTEGRAL DOMAIN
MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE,
WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING SITES FOR
CYTOSKELETAL AND OTHER PROTEINS (BY SIMILARITY).
-!- SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY
                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. IN THE
BASOLATERAL MEMBRANE OF INTERCALATED CELLS OF DISTAL TUBULES AND
COLLECTING DUCTS.
                                                                                                                                                                                                                                                                                                                                   MEDLINE-Oscostor, ...
Kudrycki K.E., Shull G.E.;
"Primary structure of the rat kidney band 3 anion exchange protein
                                                                                                                                                                      01-NOV-1991 (Rel. 20, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1).
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         Length 911;
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Anion exchange; Erythrocyte;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUE SPECIFICITY: Kidney.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms-2;
         100.0%; Score 112; DB 1; 100.0%; Pred. No. 3.2e-09;
       Query Match 100.0%; Score 112; D
Best Local Similarity 100.0%; Pred. No. 3.2
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P23562-2; Sequence=VSP_000455;
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InterPro; IPR003020; HCO3_cctranspt.
Pfan; PR00955; HCO3_cctranspt.
PRINTS; PR01231; HCO37RNSPORT.
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EMBL; L02943; AAA40801.1; -.
PIR; A33810; A33810.
                                                                                                                                                   PRT;
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                                                                       807 DRILLLEKPPKYHPDVPYVK 826
                                                                                                                                                                                                                                                                                                                              MEDLINE-89255254; PubMed-2722777;
                                                          1 DRILLEKPPKYHPDVPYVK 20
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P23562:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Band 3 anion transport protein (Anion exchange protein 1) (AE 1)
                                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (PROBABLE).
PALMITARE (BY SIMILARITY).
Missing (in isoform Kidney).
/FTIGH-VSP_000455.
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Kopito, R.R., Andersson M., Lodish H.F.;
"Structure and organization of the murine band 3 gene.";
J. Biol. Chem. 262:8035-8040(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1987) to the EMBL/GenBank/DDBJ databases.
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                  CYTOPLASMIC (POTENTIAL).
MEMBRANE (ANION EXCHANGE).
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Kopito R.R., Lodish H.F.;
"Structure of the murine anion exchange protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 108; DB 1;
Pred. No. 1.3e-08;
splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   929 AA.
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                                                                                                      POTENTIAL.
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MEDLINE-85268011; PubMed-2410791;
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SEQUENCE OF 11-929 FROM N.A.
MEDLINE-86274622; PubMed=3015590;
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Best Local Similarity 95.0
Matches 19; Conservative
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Nature 316:234-238(1985).
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SLC4A1 OR AE1.
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P04919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopito R.R.
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                                                                                                                                                        FUNCTION: BAND 3 IS THE MAJOR INTEGRAL GIYCOPROTEIN OF THE ERYTHROCYTE MEMBRANE. BAND 3 HAS TWO FUNCTIONAL DOMAINS. ITS INTEGRAL DOMAIN MEDIATES A 1:1 EXCHANGE OF INORGANIC ANIONS ACROSS THE MEMBRANE, WHEREAS ITS CYTOPLASMIC DOMAIN PROVIDES BINDING
                                                                                                                                                                                                                                   SUBUNIT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                        "Major proteolytic fragments of the murine band 3 protein as obtained
                                                                       SEQUENCE OF 33-47; 360-375; 382-395 AND 578-590.
MEDLINE-89229233; PubMed-2713407;
Raida M., Wendel J., Kojro E., Fahrenholz F., Fasold H., Legrum B.,
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J., Cloe L., Rovera G., Curtis P.J.; "Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. . .) (PROBABLE).
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HSSP, P02730, 1BTS.

HGD, MGI: 109393; 317-41.

InterPro: IPR003177, Anion_exchange.

InterPro: IPR003177, Anion_exchange.

InterPro: IPR003177, Anion_exchange.

InterPro: IPR003177, HC03_cotranspt.

Pfam, PF00955; HC03_cotranspt.

PROM: PR00315; HC03_TRNSPORT.

IIGRAMS; TIGR00314; ae; 1.

PROSITE; PS00219; ANION_EXCHANGER_1; 1.

PROSITE; PS00210; ANION_EXCHANGER_2; 1.

ITROMASTER: PS00210; ANION_EXCHANGER_2; 1.

ITROMASTER: PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                           SITES FOR CYTOSKELETAL PROTEINS, GLYCOLYTIC ENZYMES, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
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MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: ERYTHROCYTE. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                   IsoId=P04919-2; Sequence=VSP_000454;
                                                                                                                                                                                                                                                                                               Name=Erythrocyte;
IsoId=P04919-1; Sequence=Displayed;
                                                                                                                                   after in situ proteolysis.";
Biochim. Biophys. Acta 980:291-298(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X02677; CAA26506.1; -. EMBL; M29379; AAA37187.1; -. EMBL; J02756; AAA37278.1; -. EMBL; X03917; CAA27555.1; -.
                                     band 3-like protein.";
EMBO J. 5:1205-1214(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4443
4475
5529
5500
6621
6642
6678
6678
7337
7337
7398
824
883
                                                                                                                                                                                                                                                                                                                        Name=Kidney;
                                                                                                                                                                                                                        HEMOGLOBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lipoprotein;
                                                                                                              Passow H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNT: A DIMER IN SOLUTION, IT SPANS THE MEMBRANE ASYMMETRICALLY AND APPEARS TO BE TETRAMERIC.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: BRYTHROCYTE.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACROSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Band 3 anion transport protein.
Gallus gallus (Chiken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                               Gaps
                                                                                                                                                               ö
                                                                                                                     Score 108; DB 1; Length 929;
Pred. No. 1.3e-08;
                    79 Missing (in isoform Kidney).

/FTIGH-VSD 000454.

103135 MW; 5C0B281C394FB614 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Anion exchange; Erythrocyte.
1 416 CYTOPLASMIC (POTENTIAL).
DOMAIN 417 922 MEMBRANE (ANION EXCHANGE).
TRANSMEM 417 437 • POTENTIAL.
                                                                                                                                                               0; Indels
    PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                        922 AA.
                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF000955; HC03_cotransp; 1.
PRINTS; PR01231; HC03TRNSPORT.
TIGREAMS; TIGR00834; ass; 1.
PR0SITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HC03_cotranspt.
                                                                                                                                                                                                                        1 DRILLEKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                 14, Created)
                                                                                                                     96.4%;
95.0%;
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                                                                                                                                                               19; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
  861
                                                                                929 AA;
                                                                                                                                        est Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
861
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450
473
504
536
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P15575;
LIPID'
VARSPLIC
                                                                              SEQUENCE
                                                                                                                       Query Match
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B3AT_CHICK
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IsoId=P13808-1; Sequence=Displayed;
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Best Local Similarity
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   SO SET THE FET THE SET                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUB-Stomach;
MEDLINE-90094439; PubMed=2294114;
Kudrycki K.E., Newman P.R., Shlul G.E.;
Rudrycki R.E., Newman P.R., Shlul G.E.;
"CDNA cloning and tissue distribution of mRNAs for two proteins that are related to the band 3 Cl-/HCO3-exchanger.";
J. Biol. Chem. 265:462-471(1990).
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
SLC4A2 OR AE2 OR B3RP2.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kopito R.R.;

"Functional expression and subcellular localization of an anion exchanger cloned from choroid plexus.";

Proc. Natl. Acad. Sci. U.S.A. 87:5278-5282(1990).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
-!- SUBCELBUIAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindsey A.E., Schneider K., Simmons D.M., Baron R., Lee B.S.,
                                                                                                                                                                                                                                              Score 82; DB 1; Length 922;
Pred. No. 0.00011;
 EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                                                                                                                      4; Indels
                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1234 AA.
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                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
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                   POTENTIAL
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
TIGRFAMS; TIGR00834; ae; 1.
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                                                                                                                                                                                                                                              73.2%;
78.9%;
                                                                                                                                                                                                             102223
                                                                                                                                                                                                                                                                  Local Similarity 78.9
hes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                       671
691
730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134911; A34911.
P02730; 1BTQ.
                                                                                                                                                                                                             922 AA;
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LK; A34911;
HSSP; POTT
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                                                       FRANSMEM
                                                                                                                                                                                         CARBOHYD
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                                                                                                                                  TRANSMEN
                                                                            DOMAIN
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B3A2_RAT
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Gaps
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P13808; Q9ES10; Q9ES11; Q9ES12; Q9ES13;
01-JNN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Annon exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HISTAGE.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

PALMITATE (BY SIMILARITY).

G -> A (IN REF. 2).

R -> IG (IN REF. 2).

M -> I (IN REF. 2).

M -> I (IN REF. 2).
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Alper S.L., Kopito R.R., Libresco S.M., Lodish H.F.;
Cloning and characterization of a murine band 3-related cDNA from kidney and from a lymphoid cell line.";
J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lecanda J., Urtasun R., Medina J.F.; ^{\circ} "Molecular cloning and genomic organization of the mouse AE2 anion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
MEDLINE-20462926; PubMed-11006093;
                                               Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE
- DISTRIBUTION.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; DB 1; Length 1234; Pred. No. 0.0025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                   POTENTIAL. EXOPLASMIC LOOP (POTENTIAL)
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                                                                                                                   MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
PROSITE; PS00219; ANION_EXCHANGER_1; 1. PROSITE; PS00220; ANION_EXCHANGER_2; 1. Transmembrane; Glycoprotein; Transport; Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
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                                                                      Anion exchange; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136635
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                                                                                                                                                                                                                                                                                                                                       1003
1050
1129
1192
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866
878
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NCBI_TaxID=9986;
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                                                                                                                                                                                                                                                                                                                 SLC4A2 OR AEZ
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                            CONFLICT
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                                                                       Query Match
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                                                                                                                                                                                                                 B3A2_RABIT
                                                                                                                                                        qq
                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                           TISSUE SPECIFICITY: Isoform a is widely expressed at similar rISSUE SPECIFICITY: Isoform a is widely expressed at similar levels in all tissues examined. Isoforms bl and b2 are predominantly expressed in stomach although they are also detected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Missing (in isoform C1).
/FIId=VSP_000460.
ERTSPSPPTGTPHQEAAPRASKGAQTG -> MPAFQEWKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -> MDFLLRPQ (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId=VSP_000457.
MSSAPRRPASGADSLHT -> MTQ (in isoform Bl).
/FTId=VSP_000458.
                                                                                                                                                     at lower levels in other tissues. Isoform of is stomach-specific. Isoform of is expressed at slightly higher levels in lung and stomach than in other tissues.

SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS, PR01231; HULLINGER 1.
FRINTS, PR01231; HULLINGER 1.
FROSITE; PS00219; ANION EXCHANGER 1; 1.
PROSITE; PS00220; ANION EXCHANGER 2; 1.
FROSITE; PS00220; ANION EXCHANGER 2; 1.
FRANSMEMbrane; Glycoprotein; Palmitate; Alternative splicing.
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

Outpolasmin 1 703
MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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           IsoId=P13808-2; Sequence=VSP_000458;
                                         IsoId=P13808-3; Sequence-VSP_000457;
                                                                    IsoId=P13808-4; Sequence=VSP_000460;
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InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF255774; AGG23155.1; -.
EMBL; AF255774; AAG23156.1; -.
EMBL; AF255774; AAG23158.1; -.
EMBL; AF255774; AGG23157.1; -.
PIR; A31789; A31789.
                                                                                                                                                                                                                                                                                                                                            EMBL; J04036; AAA65505.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:109351; Slc4a2.
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                            Name-B2
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VARSPLIC
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                                                                                                                                                                                             ö
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (B3RP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLUIAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00219; ANION EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Iransmembrane; Glycoprotein; Transport; Antiport; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NOW Zealand white;
MPDILINE-93035730; Pubmed-1415547;
Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"Chow A., Dobbins J.W., Aronson P.S., Igarashi P.;
"CDNA Cloning and localization of a band 3-related protein from
GLREEAVFGAHGCSVCR (in isoform C2).
                                                                                                                                                                                          ;
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-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                    Length 1237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. EXOPLASMIC LOOP (POTENTIAL).
                                                                                                                                                                                             4; Indels
                      /FTId=vSP_000461.
A -> G (IN REF. 2).
W; 1A0782C0071782EE CRC64;
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MEMBRANE (ANION EXCHANGE)
POTENTIAL.
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                                                                                                                                 DB 1;
0.0025;
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                                                                                                                                    Score 74;
Pred. No. (
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PIR; A56764; A56764.
HSSP: P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
                                                                                                                                                                                                                                                                           1 DRILLLEKPPKYHPDVPYVK 20
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PRINTS; PR01231; HC03TRNSPORT.
                                                   205 A -
136813 MW;
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                                                                                                                                 Query Match 66.1%;
Best Local Similarity 65.0%;
Matches 13; Conservative
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                                                   205 20
1237 AA;
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ALTERNATIVE PRODUCTS:
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MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=12477932;

MEDLINE-22388257; PubMed=124.77932;

MEDLINE-22388257; PubMed=124.77932;

MEDLINE-22388257; PubMed=124.77932;

MEDLINE-22388257; PubMed=124.77932;

MEDLINE-22388257; PubMed=124.77932;

MEDLINE-224.8 MEDLINE N. M. Farmer A.A.; Medne L., Mellah F., Mellah P. M., Mellah P. M., Mellah P. J., Mellah M. M., Garcia A.M., Garcia A.M., Galbs R.A., Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah M. Mellah Mell
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P04920; Q969L3;
13-ANG-1987 (Rel. 05, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (BND3L).
SLC4A2 OR AEZ OR EPB3L1 OR HKB3 OR MPB3L.
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 375-1241 FROM N.A.
MEDLINE-86274622; PubMed-3015590;
Demuth D.R., Showe L.C., Ballantine M., Palumbo A., Fraser P.J.,
Cioe L., Rovera G., Curtis P.J.;
"Cloning and structural characterization of a human non-erythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PALMITATE (BY SIMILARITY).
WW. 2811D11051552BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A).
MEDLINE-92223115; PubMed-1562608;
Gehrig H., Mueller W., Appelhans H.;
"Complete nucleotide sequence of band 3 related anion transport
                                                                                                                                                                               ;
0
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EMBO J. 5:1205-1214(1986).
-!- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN OF WIDE DISTRIBUTION.
                                                                                                                                             Length 1237;
                                                                                                                                                                                4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                               Score 74; DB 1;
Pred. No. 0.0025;
                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1130:326-328(1992).
                  PRO-RICH.
HIS-RICH.
                                                                                                                                                                                                                                :|: || |||:||| |||
1133 ERLHLLLMPPKHHPDVTYVK 1152
                                74 88 HIS-1
855 855 N-LII
864 864 N-LII
878 878 N-LII
1169 1169 PALM
1237 AA; 136535 MW;
                                                                                                                                                                                                               1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein AE2 from human kidney
                                                                                                                                             66.1%;
65.0%;
                                                                                                                                                                                13; Conservative
                                                                                                                                          Ouery Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                               CARBOHYD
CARBOHYD
CARBOHYD
                                                                                              LIPID
TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                           B3A2_HUMAN
                                                                                                                                                                                                                                                                                            RESULT
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SUBCELLULAR LOCATION: Integral membrane protein.

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E -> M (IN REF. 1).
E -> A (IN REF. 1).
D -> G (IN REF. 1).
Q -> R (IN REF. 1).
E -> R (IN REF. 1).
E -> R (IN REF. 1).
L-> V (IN REF. 1).
L-> V (IN REF. 1).
L-> V (IN REF. 1).
LLGHHHGGGAESDPHVTEPLMGGVPE -> CWGITMVRGLR
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
MSSAPRLPAKGADSFCT -> MTQ (in isoform B1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EL -> DV (IN REF. 1 AND 3).
AAGAAEDDPLRRTGRP -> RQGQLKMIPSADGAA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primm,
Primm,
Primms,
Primms,
TIGRROBA34; ae; 1.
TIGRFAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Palmitate; Alternative splicing.
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
Anion exchange; Lipoprotein; Palmitate; Alternative splicing.

OCTOPLASMIC (POTENTIAL).

MEMBRANE (ANION EXCHANGE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTPTSPSLSWEVFLR (IN REF. 3).
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                                                                                                           ISOId-P04920-2; Sequence-VSP_000456;
-1. SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REF. 1 AND 3).
Q -> R (IN REF. 1 AND 3).
L -> P (IN REF. 1 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 109280; -.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0006820; F:anion transport; TAS.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003177; Anion_exchange.
InterPro; IPR003209; HCO3_cotranspt.
PRM:0955; HCO3_cotranspt.
PRN:0555; HCO3_cotranspt.
Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                   IsoId=P04920-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL. POTENTIAL.
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EMBL, BC009434; AAH09434.1; --
EMBL, X03918; CAAZ7556.1; --
FIR, S21086; S21086.
HSSP; P02730; IBTO.
Genew; HGNC.11028; SLC4A2.
                                                                                                                                                                                                                                                                                                                                                                 EMBL; X62137; CAA44067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
74
122
157
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1010
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902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1163
                                                                                         Name=B1;
                                              Name=A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
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B3A3_MOUSE
CARBOHYD
CARBOHYD
CARBOHYD
                                              SEQUENCE
                                                                      Query Match
                                                                                                                                                                             RESULT 10
B3A3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                  LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the Ewe by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                             ö
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                         16-ocr-2001 (Rel. 40, Created)
16-ocr-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 2 (Non-erythroid band 3-like protein) (AE2
                                                                                                                                                                                                                                              Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Transport; Antiport; Ion transport;
Lipoprotein; Palmitate.
                                             ö
                    Length 1241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXOPLASMIC LOOP (POTENTIAL). POTENTIAL.
                                             4; Indels
136966 MW; B116908C5A71DB77 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLUTAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                    Score 74; DB 1;
Pred. No. 0.0026;
                                                                                                                                                      PRT; 1238 AA
                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP: P02730; 1BTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR00170; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
TIGRPAMS; PR01211; HCO3_TRNSPORT.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00219; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
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PRO-RICH.
HIS-RICH.
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                                                                                 .1 DRILLLFKPPKYHPDVPYVK 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF121253; AAD19700.1; -.
                      66.1%;
65.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein;
                                             13; Conservative
                                                                                                                                                      STANDARD;
 1241 AA;
                                  Best Local Similarity
                                                                                                                                                                                                                         anion exchanger).
                                                                                                                                                                                                                                                                                   NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anion exchange;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                    SLC4A2 OR AE2
                                                                                                                                                    B3A2_CAVPO
Q9Z0S8;
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TRANSMEM
TRANSMEM
SEQUENCE
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TRANSMEM
                       Query Match
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                                             Matches
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                                                                                                                                              ö
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
       N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
PALMITATE (BY SIMILARITY).
MW; FA1739862ED5ADBF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kopito R.R., Lee B.S., Simmons D.M., Lindsey A.E., Morgans C.W.,
                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morgans C.W., Koplto R.R.;
"Generation of truncated brain AE3 isoforms by alternate mRNA processing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Regulation of intracellular pH by a neuronal homolog of the erythrocyte anion exchanger."; Cell 59:927-937(1989).
                                                                                                            Score 73; DB 1; Length 1238;
Pred. No. 0.0036;
                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId-P16283-3; Sequence-VSP_000466, VSP_000467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P16283-2; Sequence=VSP_000464, VSP_000465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- TISSUE SPECIFICITY: NEURONAL.
-1- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. cell Sci. 106:1275-1282(1993)
--- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
--- SUBCELLILLAR LOCATION: Integral membrane protein
---- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. MEDLINE-94171936; PubMed-8126106;
                                                                                                                                                                                                                                                                                                      PRT; 1227 AA.
                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=P16283-1; Sequence=Displayed;
                                                                                                            Score 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:109350; SIC4a3.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam: PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                    :|: || |||:||| ||||
1134 ERLHLLLMPPKHHPDVMXVK 1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-90075236; PubMed-2686841;
                                                                                                                                                                                1 DRILLLFKPPKYHPDVPYVK 20
856
865
879
1170
: 137358 M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M28383; AAA37184.1; -.
                                                                                                            65.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S69314; AAB30140.1; -.
                                                                                                                              65.0%;
                                                                                                                                              13; Conservative
                                                                                                                                                                                                                                                                                                      STANDARD;
        856 85
865 86
879 87
1170 117
1238 AA;
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                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=311-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=14-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=FL-AE3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schneider K.;
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NAME OF THE PART O

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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Cardiac/brain band 3-like protein) (CAE3/BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning, expression, and chromosomal localization of two isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Heart;
Kudo S., Mattei M.-G., Bloor C.M., Fukuda M., Ranney H.M., Xu A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                       HSSP; P02730; IBTQ.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR00320; HC03_corranspt.
Pfam; PF00955; HC03_corranspt.
PRINTS; PR01231; HC03_corransp; 1.
PRINTS; PR01231; HC03_CORRANSPORT.
IIGREMMs; TIGR00834; ac; 1.
PROSITE; PS000220; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
Transmembrane; Glycoprotein; Transport; Anion exchange; Lipoprotein; Palmitate.
Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
MEDLINE-55008042; PubMed-7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 68; DB 1; Length 1227; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                    MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1232 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
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POLY-SER.
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM CAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM BAE3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:||:| | |:||: |||
1125 RLLLIFMPAKHHPEQPYV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA; 135406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
                                          EMBL; J05167; AAA40798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.7%;
61.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 RILLLFKPPKYHPDVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.7
Best Local Similarity 61.1
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            868
1160
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                                                                                                                                                                                                                                                                                                                                                                                                                        .044
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                          PIR; B34911; B34911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLC4A3 OR AE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B3A3_HUMAN
P48751;
                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
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          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VSP_000464.
Missing (in isoform 311-AE3).
/FTId=VSP_000465.
/FTHMPGGDGHRGKSLN -> FCVLRSPSPCLGETVTEGKA (in isoform 14 AE3).
/FTId=VSP_000466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90094439; Pubmed-2294114;
Rudrycki K.E., Newman P.R., Shull G.E.;
Achoring and fissue distribution of mRNAs for two proteins that are related to the band 3 Cl-/HCO3-exchanger.";
                                                                                                                                                                                                                                                                                                                                                            AALIDLEQTTI -> RAFWAGNESLL (in isoform 311-AE3).
TIĞRFAMS; TICRO0834; ae; 1.
PROSITE; PSO0219; ANION_EXCHANGER_1; 1.
PROSITE; PSO0220; ANION_EXCHANGER_2; 1.
Transmembrane; Giycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate; Alternative splicing.
DOMAIN 1 707 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 1; Length 1227; Pred. No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Missing (in isoform 14-AE3).
/FTId=VSP_000467.
W: D5BEC46E03F4251C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein).
SLC4A3 OR AB3 OR B3RP3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 265:462-471(1990).

--- FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PROTEIN.
--- SUBCELLULAR LOCATION: Integral membrane protein.
--- TISSUE SPECIFICITY: UNEURONAL.
--- SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                           MEMBRANE (ANION EXCHANGE)
                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1227 AA.
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1125 RLLLIEMPAKHHPEQPYV 1142
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61.1%;
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Best Local Similarity 61.10,
Conservative
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLASMA MEMBRANE ANTON EXCHANGE PROTEIN OF WIDE
DISTRIBUTION. MEDIATES AT LEAST A PART OF THE CL(-)/HCO3(-)
EXCHANGE IN CARDIAC MYOCYTES. BOTH BAE3 AND CAE3 FORMS TRANSPORT
                                                                                                                             'Isold=P48751-2; Sequence=VSP_000462, VSP_000463;
TISSUE SPECIFICITY: BOTH BAE3 AND CAE3 ARE EXPRESSED IN FAILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Antion exchange; Lipoprotein; Palmitate; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                GO: 00009897; C:integral to plasma membrane; TAS. GO: 00005847; C:integral to plasma membrane; TAS. GO: 000005452; C:membrane fraction; TAS. GO: 00:0005452; F:inorganic anion exchanger activity; TAS. GO: 00:0006832; P:small molecule transport; TAS. InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001707; Anion_exchange.
PRINTS; PR01231; HC03_cotranspt.
PRINTS; PR01231; HC03_TRNSPORT.
IIGRRAMS; TIGR00834; ae; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Missing (in isoform CAE3).
/FTId=vSP_000462.
SPS -> MPA (in isoform CAE3).
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                                                                                                                                                             SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL). POTENTIAL).
                                                    SUBCELLULAR LOCATION: Integral membrane protein ALTERNATIVE PRODUCTS:
                                                                        Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTIG-VSP_000463.
                                                                                                        IsoId=P48751-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                   TICREAMS; TICRO0814; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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                                                                                                                     Name=CAE3;
                                                                                               Name=BAE3
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                                                                                                                                                                                                                                                             Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Transport; Antiport; Ion transport; Anion exchange; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                    B3A3_RABIT STANDARD; PRT; 1233 AA.
018917;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anion exchange protein 3 (Neuronal band 3-like protein) (Anion exchanger 3 brain isoform).
SLC4A3 OR AE3.
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                      DB 1; Length 1232;
GS -> FI (IN REF. 2).
F -> L (IN REF. 2).
A -> S (IN REF. 2).
EGSLA -> D (IN REF. 2).
S -> C (IN REF. 2).
S -> G (IN REF. 2).
R -> E (IN REF. 2).
L -> P (IN REF. 2).
I -> M (IN REF. 2).
I -> M (IN REF. 2).
I -> M (IN REF. 2).
I -> M (IN REF. 2).
                                                                                                                                                                                                                                                               Indels
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Abuladze N., Pushkin A., Kurtz I.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: PLASMA MEMBRANE ANTON EXCHANGE PROTEIN.
-!-SUBCELLULAR LOCATION: Integral membrane protein.
-!-TISSUE SPECIFICITY: NEURONAL.
-!-SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMBRANE (ANION EXCHANGE)
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                                                                                                                                                                                                                                        0.17;
                                                                                                                                                                                                                                                               Mismatches
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                    Score 62;
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InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotranspt.
PRINTS; PR01231; HCO3TRNSPORT.
                                                                                                                                                                                                                                                                                                                          1130 RLLLILMPAKHHPEQPYV 1147
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                                                                                                                                                                                                                      55.4%;
                                                                                                                                                                                 135706
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Best Local Similarity 55.0.
    813
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861
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875
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1232 AA;
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253 DEILQLETPPKYHTQIDYV 271

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Genew; HGNC:1
MIM; 606096;
                              RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: SOCS family proteins form part of a classical negative feedback system that regulates cytokine signal transduction.
-- SIMILARITY: Contains 1 SH2 domain.
-- SIMILARITY: Contains 1 SOCS box domain.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             NAC. . .) (POTENTIAL).
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2 domain; Growth regulation; Signal transduction inhibitor. DOMAIN 286 381 SH2.
                                                                                                                               Score 62; DB 1; Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.8%; Score 58; DB 1; Length 440; 57.9%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Indels
                                                                                                                                                   4; Indels
                                                                                                            AE486423E9818583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50623 MW; A4A747AB7F6FF08C CRC64;
                            N-LINKED (GLCNAC.
PALMITATE (BY SIM:
HIS-RICH.
POLY-GLU.
                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
SOCS7 OR SOCS4.
                                                                                                                                        Pred. No. 0.17;
                                                                                                                                                                                                                                            440 AA.
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          POTENTIAL. POTENTIAL.
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                                                                    POLY-SER
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                                                                                                                                                                      2 RILLLFKPPKYHPDVPYV 19
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                                                                                                                              Query Match 55.4%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                           135759
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ProDom; PD000093; SH2; 1.
SMART; SM00253; SH2; 1.
SMART; SM00253; SCS; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50225; SCS; 1.
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InterPro; IPR000980; SH2.
InterPro; IPR001496; SOCS.
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Matches 11; Conservative
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1233 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 AA;
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443
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-1- TISSUE SPECIFICITY: Not widely expressed. Predominantly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in adipose tissue.
-!- DOMAIN: CONTAINS TWO HOMOLOGOUS BUT DISTINCT CARBOHYDRATE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hotta K., Firology, Matsukawa Y., Takahashi M., Nishizawa H., Kishida K., Matsuda M., Kuriyama H., Kihara S., Nakamura T., Tochino Y., Bodkin N.L., Hansen B.C., Matsuzawa Y.; "Galectin-12, an adipose-expressed galectin-like molecule possessing apoptosis-inducing activity.";
J. Biol. Chem. 276:34089-34097(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-Retina;
MEDLINE-21283005; PubMed=11283015;
Yang R.-Y., Hsu D.K., Yu L., Ni J., Liu F.-T.;
"Cell cycle regulation by galectin-12, a new member of the galectin superfamily.";
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
LEGC_HUMAN STANDARD, PRT; 336 AA.
096DT0; Q96DS9; Q96PR9; Q9H258; Q9H259; Q9N202;
28 FFBB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Galectin-12 (Galectin-related inhibitor of proliferation).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - SIMILARITY: BELONGS TO THE GALAPTIN (S-LECTIN) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId-Q96DT0-4; Sequence-VSP_003100, VSP_003102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=6;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=B; Synonyms=GRIP1a;
IsoId=Q96DT0-2; Sequence=VSP_003100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q96DT0-3; Sequence=VSP_003102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=E; Synonyms=1;
IsoId=Q96DT0-5; Sequence=VSP_003099;
Name=F; Synonyms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS B; E AND F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q96DT0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21423969; PubMed=11435439;
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EMBL; AF310686; AAG40863.1;
EMBL; AF310687; AAG40864.1;
EMBL; AF222695; AAF34677.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF244976; AAK77330.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissue=Adipose tissue;
                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                   LGALS12 OR GRIP1.
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46.4%; Score 52; DB 1; Length 336;
Best Local Similarity 57.1%; Pred. No. 1.4;
Matches 8; Conservative 3; Mismatches 3; Indels
InterPro; IPR001079; Galectin.
Pfam; PF00337; Gal-bind_lectin; 1.
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Search completed: September 3, 2003, 11:46:59 Job time: 11.25 secs

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RESULT 1
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Ogxsw5 bos taurus

Ogos79 gallus gall

Ogft99 pallus gall

Ogft95 oncorhynchu

Ogft52 oncorhynchu

Ogft52 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu75 sus scrofa

Ogfu76 pallus gall

Oguey6 homo sapien

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                                                                                  September 3, 2003, 11:40:18 ; Search time 44.5 Seconds
(without alignments)
115.979 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
                                                        OM protein - protein search, using sw model
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Perfect score:
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O9erp4 mus musculu O9erp5 mus musculu O9udj1 homo sapien O99416 homo sapien O13717 homo sapien O95xv2 drosophila O81qd4 drosophila O81qd5 drosophila O81qd5 drosophila O95233 homo sapien O8cfs3 mus musculu O96xt0 mus musculu O96xt0 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O89xv6 mus musculu O80xv7 mus musculu	ratts ratts ratt ratt
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ALIGNMENTS

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	AA.			Last sequence update)	Last annotation update)			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Sciurognathi; Muridae; Murinae; Rattus.						"Molecular cloning and characterization of band 3 anion exchange		Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.									E4B200780CB07D3A CRC64;	Score 104; DB 11;	.6e-08;	s 0;			
	849 AA.		_	quence	notati			ata; V	ognath	1					tion o	••	nBank/							. 1.	. 1.	00780CI	104;	No. 3	Mismatches			
	PRT;		Created)	ast se	last an	÷		Crani	Sciur					V.M.;	teriza	protein (AE1) mRNA from rat colon.";	MBL/Ge		InterPro; IPR001717; Anion_exchange.	InterPro; IPR003020; HCO3_cotranspt.	-;	.:		PS00219; ANION_EXCHANGER_1;	NGER_2	E4B2	Score	Pred.	0; Misr	. 20		677
	Ι,		19,	19,	. 23, I	proteir		ordata;	Rodentia;					jendrar	charac	n rat c	the F	33.1;	ojon_ex	303_cot	transp;	RNSPORT	e; 1.	N_EXCH?	N_EXCH!	94312 MW;	100.08;	100.0%;		THANALI	= = =	LHANALT
	PRELIMINARY;		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	Band 3 anion exchange protein.	Rattus norvegicus (Rat).	oa; cho	ia; Ro			Α.		Ye H., Binder H.J., Rajendran V.M.;	ng and	NA from	001) to	AAK387.	717; A	020; HC	Pfam; PF00955; HCO3_cotransp;	PRINTS; PR01231; HCO3TRNSPORT.	TIGRFAMS; TIGR00834; ae; 1.	; ANIO	; ANIOI	A; 94.			Conservative	GMPWLSATTVRSVTHANALT		658 GMPWLSATTVRSVTHANALT
	PREI				33 (Tre	ion exc	rvegicu	: Metaz	Euther)=10116		FROM N.	lon;	nder H.	r cloni	AE1) MF	(APR-2	30082;	IPR001	IPR003	3955; F	301231;	TIGROC	5800219	S00220	849 AA;		Lmilari		SMPWLSA	= = =	MPWLSA
	Q912E7	0912E7;	01-DEC-2001	01-DEC-2001	01-MAR-2003	d 3 and	tus no	aryota;	Mammalia; Eutheria;	NCBI_TaxID=10116;		SEQUENCE FROM N.A.	TISSUE=Colon;	H., Bir	lecular	tein (A	mitted	L; AYO	erPro;	erPro;	m; PF0(NTS; PI	RFAMS;	PROSITE; I	PROSITE; I	SEQUENCE	Match	Best Local Similarity	s 20;	1	_	929
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                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Kidney;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF163028; AAD43354-1;

HISSP; P02730; 1BNX.

InterPro; IPR001717; Anion_exchange.

InterPro; IPR003020; HC03_cotranspt.

Pfam; PP00955; HC03_cotranspt.

PRINTS; PR01231; HC03TRNSPORT.
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Koshino I., Inaba M., Matsumoto M., Ono K.;

Koshino I., Inaba M., Matsumoto M., Ono K.;

Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";

Gominant hereditary spherocytosis in cattle.";

EMBL; AFIG3826; ADA3533.1;

EMBL; AFIG3826; ADA3533.1;

InterPro; IPR001717; Anion_exchange.

InterPro; IPR003020; HOO3_cotranspt.

PRINTS; PR00955; HCO3_cotranspt.

PRINTS; PR01231; HCO3TENSPORT.
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                                                                                                                                                                                                                           Bos taurus (Bovine).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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95.0%; Pred. No. 1.1e-07;
.ive 1; Mismatches 0; Indels
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 930 AA; 104374 WW; 4F6AADFEBAF6A3A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Band 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 95.0
                                PRELIMINARY;
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                             09TUQ0
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Q9XSW5
Q9TUQ0
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Erythroid anion transporter.
Eathbroid anion transporter.
Eallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cox J.V., Lazarides E.;
"Alternative primary structures in the transmembrane domain of the chicken erythroid anion transporter.";
Mol. Cell. Biol. 8:1327-1335(1988).
EMBL; M19496; AAA48604.1; -.
HSSP; P02730; 1BTQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 812;
                     Length 930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kimberley A.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL604064; CAD43432.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
SI:d2180G5.1 (novel solute carrier protein) (Fragment).
SI:D2180G5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001717; Anion_exchange.
InterPro; IPR001717; Anion_exchange.
InterPro; IPR001201; HCO3_cotranspt.
FIGN095; HCO3_cotranspt. 1.
FIGNFAMS; PG01231; HCO3TRNSPORT.
IGRPAMS; TIGR00834; ae; 1.
FROSTITE; PS00219; ANION_EXCHANGER_1; 1.
SEQUENCE 844 AA; 93808 MW; C463F993D5974276 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                812 AA; 91488 MW; 855A5600C91E3073 CRC64;
Score 101; DB 6; L. Pred. No. 1.2e-07;
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                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                 738 GMPWLSATTVRTVTHANALT 757
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                                                                                                                      1 GMPWLSATTVRSVTHANALT 20
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                     97.1%;
95.0%;
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                            Best_Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus.
NCBI_TaxID=9031;
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TISSUE-Stomach;
MEDLINE=9639307; PubMed-8756692;
ACOLOTARE-9639307; Chernova M.N., Yannoukakos D., Alper S.L.;
"Proteolytic cleavage sites of native AE2 anion exchanger in gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                         Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 466;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC002234, 13.  
MGD; MGI:109351; Slc4a2.  
InterPro; IPR001717; Anion_exchange.  
Interpro; IPR003020; HGO3_cotranspt.  
Pfam; PF00955; HGO3_cotranspt.  
PRINTS; PR01231; HGO3TRNSPORT.
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103 103
103 AA; 11012 MW; 29A99247E768B455 CRC64;
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SEQUENCE 466 AA; 52003 MW; 481C1108E28D03B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.0 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                097075;
01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAX-2003 (TrEMBLrel. 23, Last annotation update)
Chloride-bicarbonate anion exchanger AE2 (Fragment)
                                                                                                                      Query Match 89.4%; Score 93; DB 11; La
Best Local Similarity 85.0%; Pred. No. 2.4e-07;
Matches 17; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.4%; Score 93; DB 11;
85.0%; Pred. No. 1.2e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  466 AA
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PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Biochemistry 35:10367-10376(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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      NON_TER
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SEQUENCE
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Q99LT5;
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Q9TU75
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MEDLINE-96080151; PubMed-7489705;
Fievet B., Gabillat N., Borgese F., Motais R.;
Expression of band 3 anion exchanger induces chloride current and taurine transport: structure-function analysis.";
EMBO J. 14:5158-5169(1995).
EMBL; Z50848; CAA90701.1; -.
HSSP; P02730; 18FQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oncorpynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cynomys ludovicianus (Black-tailed prairie dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
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Abedin Z.R., Moser A.J., Roslyn J.J., Abedin M.Z.;
"Expression of anion exchange protein 2 (AE-2) in gallbladder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 95; DB 13; Length 912;
Pred. No. 1.1e-06;
1; Mismatches 1; Indels
                                 Indels
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF012095; AAB66033.1;
InterPro; IFR0031020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotransp; 1.
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FIGREAMS; TIGRO0834; ae; 1.

PROSITE; PS00219; ANION_EXCHANGER_1; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.

PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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L Similarity 90.0%; Pred. No. 9.8e-07; 18; Conservative 1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                912 AA
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InterPro; IPR003020; HCO3_cotranspt.
Pfan; PF00955; HCO3_cotransp; 1.
PRINTS; PR01231; HCO3TRNSPORP.
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90.0%;
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nes 18; Conservative
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Best Local Similarity
Matches 18; Conserv
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Best Local S
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SEQUENCE FROM N.A.
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                                                                                                              NCBI_TaxID=9031;
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                                                                                Zolotarev A.S., Shmukler B.E., Alper S.L.;
"AEZ anion exchanger polypeptide is a homooligomer in pig gastric membranes: a chemical cross-linking study.";
Biochemistry 38:8521-8531(1999).
EMBL; AF120099; AAF00977.1; -.
HSSP; P02730; 1BTQ.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUNAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
21-JUN Experiment of Solution and Solution exchanger, member 2
(Erythrocyte membrane protein band 3-11ke 1).
Homo sapiens (Human).
Homo sapiens (Human).
Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBL_TaxID-9606;
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85.0%; Pred. No. 3e-06;
tive 2; Mismatches 1; Indels
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TIGRRAMs; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; P000220; ANION_EXCHANGER_2; 1.
SEQUENCE 1159 AA; 127747 MW; 9F083A2BEBFF5D74 CRC64;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028601; ARH28601.1; -
Interpro; IPR00117; Anion_exchange.
Interpro; IPR0032020; HC03_cotranspt.
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InterPro; IPR003020; HCO3_cotranspt.
Pfiam; PF00955; HCO3_cotranspt.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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                          TISSUE-Stomach;
MEDLINE-99315230; PubMed-10387099;
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nes 17; Conservative
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUB-Proventriculus;
MEDLINE-96224107; PubMed-8621532;
MEDLINE-96224107; PubMed-8621532;
COX K.H., Adair-Kirk T.L., Cox J.V.;
"Variant AE2 anion exchanger transcripts accumulate in multiple cell types in the chicken gastric epithelium.";
J. Biol. Chem. 271:8895-8902(1996).
BIOL. Chem. 271:8895-8902(1996).
HSSP: P02730; IBTQ.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR001707; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt. 1.
PRINTS; PR01231; HCO3TRNSPORT. 1.
TIGRPAMS; TIGR00834; ae; 1.
TIGRPAMS; TIGR00834; ae; 1.
PROSITE; PS002129; ANION_EXCHANGER_1; 1.
SEQUENCE 1219 AA; 135288 WW; 25F42A73C3483B21 CRC64;
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Interpro; IPR0017019, HCO3_cotranspt.
Pfam: PF00955; HCO3_cotranspt.
PRIGHS; PR01231; HCO3_CTRNSPORT.
TIGREAMS; TIGR00834; ae; 1.
PROSTIE; PS00219; ANION_EXCHANGER_1; 1.
PROSTIE; PS002205, ANION_EXCHANGER_2; 1.
SEQUENCE 1227 AA; 135577 WW; 5D47714C17FB8EF7 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Anion exchanger 2 type b1.
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85.0%; Pred. No. 3.1e-06;
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Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
BMB.; U62531; AAC50964.1; -.
                                                                                InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HCO3_cotranspt.
Pfam; PF00955; HCO3_cotranspt.
PR01231; HCO3_TRNSPORT.
IIGRFAMS; TIGR00834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 137009 MW; D266ECDAB238FD97 CRC64;
  MEDLINE-97179202; PubMed-9027488;
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"Tissue-specific.N-terminal isoforms from overlapping alternate promoters of the human AE2 anion exchanger gene.";

Blochem. Biophys. Res. Commun. 267:228-235(2000).

EMBL; U76669; AAF23240.1; -.

R EMBL; U76669; AAF23240.1; JOINED.

R EMBL; U76669; AAF23240.1; JOINED.

R HSSP; PO2730; IBTQ.

InterPro; IPR00177; Anion_exchange.

InterPro; IPR00177; Anion_exchange.

R Pfam; PF00955; HGO3_cotranspt.

R Pfam; PF00955; HGO3_cotranspt.

R TIGRRAMS; TIGRO0834; ae; 1.

R PROSITE; PS00220; ANION_EXCHANGER_1; 1.

R PROSITE; PS00220; ANION_EXCHANGER_2; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
"Molecular cloning and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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85.0%; Pred. No. 3.2e-06;
ive 2; Mismatches 1; Indels
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89.4%;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=97179202; PubMed=9027488;
Medina J.F., Acin A., Prieto J.;
Modina J.E., Acin A., Prieto J.;
Molecular clonding and characterization of the human AE2 anion exchanger (SLC4A2) gene.";
Genomics 39:74-85(1997).
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  Length 1241;
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Score 93; DB 4; Length 124
Pred. No. 3.2e-06;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGNOMS: TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 1241 AA; 136980 MW; D2FDA72E20D70D64 CRC64;
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                                                                                                                                                                                                                                                                                         01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 89.4%; Score 93; DB 4; Le Best Local Similarity 85.0%; Pred. No. 3.2e-06; Matches 17; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001717; Anion_exchange.
InterPro; IPR003020; HGO3_cotranspt.
Pfam; PF00955; HGO3_cotranspt.
PRINTS; PR01231; HGO3TRNSPORT.
                                                                                                                 1050 GLPWLAAATVRSVTHANALT 1069
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    89.4%;
                                                                                                                                                                                                                                                                                                                                                              Anion exchanger 2 type a.
  Query Match 89.4
Best Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
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Search completed: September 3, 2003, 11:50:01 Job time : 46.5 secs

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NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               091ZE7
                                                                                    GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match,100%
Listing first 45 'summaries
                                                         OM protein - protein search, using sw model
                                                                                                                                                                              1 GMPWLSATTVRSVTHANALT 20
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Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
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sp_bacteria:*
sp_fungi:*
sp_human:*
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sp_phage:*
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Maximum DB seq length: 200000000
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                                                                                                                                                               Perfect score:
                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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                                                                                                                                                                              Sequence:
                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	4	Describerou	Q91ze7 rattus norv	O9tuq0 bos taurus	Q9xsw5 bos taurus	090579 qallus qall	081ft9 brachydanio	091452 oncorhynchu	035225 cynomys lud	0991t5 mus musculu	09tu75 sus scrofa	Q8taq3 homo sapien	090710 gallus gall	Oguey4 homo sapien	Oguey5 homo sapien	099654 homo sapten	Oguevé homo sapien	P79877 lampetra ja
	£		Q91ZE7	05n160	Q9XSW5	090579.	Q8JFT9	091452	035225	Q99LT5	Q9TU75	QBTAG3	090710	Q9UEY4	Q9UEY5	099654	Q9UEY6	P79877
	g	9 :	11	9	9	13	13	13	Ξ	7	ဖ	4	13	4	4	4	4	13
	Query	יייייייייייייייייייייייייייייייייייייי	849	855	930	844	812	912	103	466	622	1159	1219	1227	1232	1241	1241	160
ф	Query	1177	100.0	97.1	97.1	96.2	91.3	91.3	89.4	89.4	89.4	89.4	89.4	89.4	4.6	89.4	89.4	85.6
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	Result	2	-	7	m	4	2	9	7	&	σ	10	11	12	13	14	. 15	16

O9erp4 mus musculu	Q9erp5 mus musculu	Q9udjl homo sapien	Q99416 homo sapien	homo	Q95sw2 drosophila	Q8mrk3 drosophila	Q8iqd4 drosophila	Q8iqd6 drosophila	Q8iqd5 drosophila	Q9vt48 drosophila	095233 homo sapien		Omor	snw 0	Q8c943 mus musculu	Q9jkv6 mus musculu	Q8jzr6 mus musculu	Q8byi7 mus musculu	094843 homo sapien	4 mus	homod	homod	Q9hc88 homo sapien	Q9y6m7 homo sapten	3 ratt	09qyd5 rattus norv		Q9vm32 drosophila
O9ERP4	Q9ERP5	Q9UDJ1	099416	013717	Q95SW2	Q8MRK3	Q81QD4	900180	Q81QD5	O9VT48	095233	Q8CFS3	900H60	Q9EST0	Q8C943	Q9JKV6	Q8JZR6	Q8BYI7	094843	Q8BWZ4	Q9UIB9	060350	O9HC88	Q9Y6M7	Q9R1N3	090YD5	Q9R1L1	Q9VM32
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85	82	85	80	80	69	69	69	69	69	69	63	63	63	63	63	63	63	63	63	59	59	59	59	53	59	59	59	28
88	83	88.5	84	84	72	72	72	72	72	72	99	99	99	99	99	99	99	99	99	62	62	62	62	62	. 62	62	62	61
17	18	19	20	. 21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Ogizer Preliminary; Pri; 849 AA.

AC 0912E7.

AC 0912E7.

CONTECTOR (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DT 01-DEC-2001 (TrEMBLrel. 23, Last annotation update)

DE Band a anion exchange protein.

OS Rattus norvegicus (Rat).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBL_TAXID-10116;

RN 1]

RR Ye H., Binder H.J., Rajendran V.M.;

RY Ye H., Binder H.J., Rajendran V.M.;

RY Ye H., Binder H.J., Rajendran V.M.;

RY Ye H., Binder H.J., Rajendran V.M.;

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RY Ye H., Binder H.J., Rajendran V.M.;

RY Ye H., Binder H.J., Rajendran V.M.;

BY You S. AN10019 AN1001 Cachange.

DR RHEL; AN103022; AN103131;

DR PROSTER; PSO0120; AN10N EXCHANGER_1; 1.

DR PROSTER; PSO0120; AN10N EXCHANGER_2; 1.

SQ SEQUENCE 849 AA; 94312 MW; E4B200780CB07D3A CRC64;

DAR PROSTER; PSO0120; AN10N EXCHANGER_2; 1.

SQ SEQUENCE 849 AA; 1000.0%; Score 104; DB 11; Length 849;

Best Local Similarity 100.0%; Pred. No. 3.6e-08;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps

Oy I GMPS

RESULT 2

q

658 GMPWLSATTVRSVTHANALT 677

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97.1%;
95.0%;
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Best Local Similarity 90.0
Matches 18; Conservative
     Query Match 97.1
Best Local Similarity 95.0
Matches 19; Conservative
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                                                                                                                                                                                          PRELIMINARY;
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NCBL_TaxID=7955;
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Koshino I., Inaba M., Matsumoto M., Ono K.;
Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated
with decreased mutant mRNA possessing dominant negative effect and
dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF165826; AAD43593.1; -.
HSSP; P02730; 1BNX.
                                                                                                                                                                                                                                             TISSUE-Kidney;
Koshino I., Inaba M., Matsumoto M., Ono K.;
Koshino I., Inaba M., Matsumoto M., Ono K.;
"Band 3 Bov. Nippon: a nonsense mutation in the band 3 gene associated with decreased mutant mRNA possessing dominant negative effect and dominant hereditary spherocytosis in cattle.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163828; AAD43354.1;
HSSP; P02730; IBNX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.1%; Score 101; DB 6; Length 85
95.0%; Pred. No. 1.1e-07;
Live 1; Mismatches 0; Indels
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PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGREAMS; TIGRO0834; ae; 1.
PROSITE; PS00219; ANION_EXCHANGER_1; 1.
PROSITE; PS00220; ANION_EXCHANGER_2; 1.
SEQUENCE 855 AA; 95643 MW; 06CD037324F69872 CRC64;
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Last annotation update)
                                             Created)
Last sequence update)
Last annotation update)
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            855 AA.
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01-NOV-1999 (TIEMBLrel. 12, Last seq
01-MAR-2003 (TIEMBLrel. 23, Last anno
Band 3 protein.
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Interpro; IPR003005; HGG3_cotranspt.
Pfam, Pf00955; HGG3_cotranspt.
PRINTS; PR01231; HGG3TRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001717; Anion_exchange.
Interpro; IPR003020; HC03_cctranspt.
Pfan; PF00955; HC03_cctranspt.
PRINTS; PR01231; HC03TRNSPORT.
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              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 GMPWLSATTVRTVTHANALT 682
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                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.1
Best Local Similarity 95.0
Matches 19; Conservative
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            PRELIMINARY;
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                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                Band 3 protein.
                               Q9TUQ0;
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               09TU00
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Q9XSW5
09TU00
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MEDLINE-8016609; PubMed-2035670;

COX J.V. tazarides E.;

C
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Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2002 (TrEMBLrel. 22, Created)
01-MR-2003 (TrEMBLrel. 23, Last sequence update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
01-MR-2003 (TrEMBLrel. 23, Last annotation update)
01:02180G5.1 (novel solute carrier protein) (Fragment).
01:02180G5.1.
02:02180G5.1.
03:02180G5.1.
04:02180G5.1.
05:02180G5.1.
06:02180G5.1.
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07:02180G5.1.
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Score 101; DB 6; Length 930;
Pred. No. 1.2e-07;
1; Mismatches 0; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL604064; CAD43432.2; -.
NON_TER 1 1 1 100 um. 85585600C91E3073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91488 MW; 855A5600C91E3073 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 100; DB 13;
Pred. No. 1.6e-07;
; Mismatches 0;
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